

Fig.1.

Sequence ID 1

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1  TGGC AGG GGT GCA AGG AGT TCT TCA GGC GGA GTG TAA CCA AAA ATG
   ACGC TCC CCA CGT TCC TCA AGA AGT CCG CCT CAC ATT GGT TTT TAC

46 CAG TGT ACA TAT GCA AAT TCG GCC ATG CTT GCG AAA TGG ATA TGT
   GTC ACA TGT ATA CGT TTA AGC CGG TAC GAA CGC TTT ACC TAT ACA

91 ATA TGC GGA GAA AAT GCC AAG AGT A
   TAT ACG CCT CTT TTA CGG TTC TCA T
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Fig.2.

Sequence ID 2

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      3      9      15      21      27      33      39      45
      |      |      |      |      |      |      |
1  TCC ACT GGT GTT TTC ACC ACC ACA GAA AAG GCC TCT GCT CAT TTA
   AGG TGA CCA CAA AAG TGG TGG TGT TTT TTC CGG AGA CGA GTA AAT

46 GAG GGT GGT GCT AAG AAG GTC ATC ATC TCC TGC TGC CCA GCG CTG
   CTC CCA CCA CGA TTC TTC CAG TAG TAG TAG AGG ACG GGT CGC GAC

91 ACC CAT GTT CGT CGT TGG TGT CAA CCT TGA AGC AGT ATG ACC CCT
   TGG GTA CAA CAA GCA ACC ACC ACA GTT GGA ACT TCG TCA TAC TGG GGA

136 CTT ACA AGG TCA TCT CCA ACG CCT CCT GCA CAA CCA ACT GGC GCC TCG
   GAA TGT TCC TCC AGT AGA GGT TGC TGC GGA CGT GGT TGA CGG AGC

181 CTC CTC TCG CTA AGG TCA TCC ATG ACA ACT TCG AGA TCA TTG AAG
   GAG GAG AGC GAT TCC AGT AGG TAC TGT TGA AGC TCT AGT AAC TTC

226 GTC TGA TGA CCA CTG TAC ACG CCA CCA CTG CCA CCC AGA AGA CAG
   CAG ACT ACT GGT GAC ATG TGC GGT GGT GAC GGT GGT TCT TCT GTC

271 TGG ATG GAC CCT CTG GTA AAC TGT GGC GTG ATG GCC GTG GTG CTC
   ACC TAC CTG GGA GAC CAT TTG ACA CCG CAC TAC CGG CAC CAC GAG

316 AGC AGA ATA TCA TTC CCG CGG AAT TCC CCA GCC GCA GCT AGC TAA
   TCG TCT TAT AGT AAG GGC GCC GCC TTA AGG GGT CGG CGT CGA TCG ATT
```

Fig.2 i.

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361 CCT GCA GCA GAC ACA ACC CCT ACC TTC CAT GCC GTT ACC AAT GCC
    GGA CGT CGT CTG TGT TGG GGA TGG AAG GTA CGG CAA TGG TTA CGG

406 ACC GAC AAC ACC CAA ATC AGA AAA CGA GTC AAT GTC ATC AGG TCG
    TGG CTG TTG TGG GTT TAG TCT TTT GCT CAG TTA CAG TAG TCC AGC

451 TGA GGA ACT GTC TCC AGC TTC GAG TGT AAA CGG CTG CAG CAC AGA
    ACT CCT TGA CAG AGG TCG AAG CTC ACA TTT GCC GAC GTC GTG TCT

496 TGG CGA GGC GAG GCG GCA GAA AGG CCC AGC GCC GAG GCA GCA
    ACC GCT CCG CTC CGC CGT CTT CTT TCC GGG TCG CGG CTC CGT CGT

541 AGA AGA GCT ATG TCT TGT CTG CGG CGA CAG AGC CTC CGG ATA TCA
    TCT TCT CGA TAC AGA ACA GAC GCC GCT GTC TCG GAG GCC TAT AGT

586 CTA CAA CGC GCT CAC ATG TGA AGG GTG TAA AGG TTT CTT CAG GCG
    GAT GTT GCG CGA GTG TAC ACT TCC CAC ATT TCC AAA GAA GTC CGC

631 GAG TGT AAC CAA AAA TGC AGT GTA CAT ATG CAA ATT CGG CCA TGC
    CTC ACA TTG GTT TTT ACG TCA CAT GTA TAC GTT TAA GCC GGT ACG

676 TTG CGA AAT GGA TAT CTA TAT GCG GAG AAA ATG TCA GGA GTG TCG
    AAC GCT TTA CCT ATA GAT ATA CGC CTC TTT TAC AGT CCT CAC AGC

721 GTT GAA GAA ATG TCT TGC GGT GGG CAT GAG GCC CGA GTG CGT GGT
    CAA CTT CTT TAC AGA ACG CCA CCC GTA CTC CGG GCT CAC GCA CCA

766 GCC GGA GAA CCA GTG TGC AAT GAA ACG GAA AGA GAA AAA GGC GCA
    CGG CCT CTT GGT CAC ACG TTA CTT TGC CTT TCT TCT TTT CCG CGT

```

Fig.2 ii.

811 GAG GGA AAA AGA CAA ATT GCC CGT CAG TAC GAC GAC AGT AGA CGA
CTC CCT TTT TCT TCT TAA CGG GCA GTC ATG CTG CTG TCA TCT GCT

856 TCA CAT GCC TCC CAT CAT GCA ATG TGA CCC TCC GCC CCC AGA GGC
AGT GTA CGG AGG GTA GTA CGT TAC ACT GGG AGG CGG GGG TCT CCG

901 CGC TAG AAT TCT GGA ATG TGT GCA GCA CGA GGT GGT GCC ACG ATT
GCG ATC TTA AGA CCT TAC ACA CGT CGT GCT CCA CGG TGC TAA

946 CCT GAA TGA GAA GCT AAT GGA ACA GAA CAG ATT GAA GAA CGT GCC
GGA CTT ACT ACT CTT CGA TTA CCT TGT CTT GTC TAA CTT CTT GCA CGG

991 CCC CCT CAC TGC CAA TCA GAA GTC GTT GAT CGC AAG GCT CGT GTG
GGG GGA GTG ACG GTT AGT CTT CAG CAA CTA GCG TTC CGA GCA CAC

1036 GTA CCA GGA AGG CTA TGA ACA ACC TTC CGA GGA AGA CCT GAA GAG
CAT GGT CCT TCC GAT ACT TGT TGG AAG GCT CCT TCT GGA CTT CTC

1081 GGT TAC ACA GTC GGA CGA GGA CGA AGA CTC GGA TAT GCC GTT
CCA ATG TGT CAG CCT GCT GCT CCT GCT GAG CCT ATA CGG CAA

1126 CCG TCA GAT TAC CGA GAT GAC GAT TCT CAC AGT GCA GCT CAT CGT
GGC AGT CTA ATG GCT CTA CTG CTA AGA GTG TCA CGT CGA GTA GCA

1171 AGA ATT CGC TAA GGG CCT CCC GGG CTT CGC CAA GAT CTC GCA GTC
TCT TAA GCG ATT CCC GGA GGG CCC GAA GCG GTT CTA GAG CGT CAG

1216 GGA CCA GAT CAC GTT ATT AAA GGC GTG CTC AAG TGA GGT GAT GAT
CCT GGT CTA GTG CAA TAA TTT CCG CAC GAG TTC ACT CCA CTA CTA

1261 GCT CCG AGT GGC TCG GCG GTA TGA CGC GGC CAC CGA CAG CGT ACT
CGA GGC TCA CCG AGC CGC CAT ACT GCG CCG GTG GCT GTC GCA TGA

Fig.2 iii.

1306 GTT CGC GAA CAA CCA GGC GTA CAC TCG CGA CAA CTA CCG CAA GGC
CAA GCG CTT GTT GGT CCG CAT GTG AGC GCT GTT GAT GGC GTT CCG

1351 AGG CAT GGC GTA CGT CAT CGA GGA CCT GCT GCA CTT CTG TCG GTG
TCC GTA CCG CAT GCA GTA GCT CCT GGA CGA CGT GAA GAC AGC CAC

1396 CAT GTA CTC CAT CAT GAT GAT GGA TAA CGT GCA TTA TGC GCT GCT TAC
GTA CAT GAG GTA CTA CTA CCT ATT GCA CGT AAT ACG CGA CGA ATG

1441 AGC CAT TGT CAT CTT CTC AGA CCG GCC CGG GCT TGA GCA ACC CCT
TCG GTA ACA GTA GAA GAG TCT GGC CGG GCC CGA ACT CGT TGG GGA

1486 GTT GGT GGA GGA CAT CCA GAG ATA TTA CCT GAA CAC GCT ACG GGT
CAA CCA CCT CCT GTA GGT CTC TAT AAT GGA CTT GTG CGA TGC CCA

1531 GTA CAT CCT GAA CCA GAA CAG CGC GTC GCC CGG GAT CCG CAC GCT GGG
CAT GTA GGA CTT GGT CTT GTC GCG CAG CGG GCC GCG GCA GTA

1576 CTT CGG CGA GAT CCT GGG CAT ACT GAC GGA GAT CCG CAC GCT GGG
GAA GCC GCT CTA GGA CCC GTA TGA CTG CCT CTA GGC GTG CGA CCC

1621 CAT GCA GAA CTC CAA CAT GTG CAT CTC CCT CAA GCT GAA GAA CAG
GTA CGT CTT GAG GTT GTA CAC GTA GAG GGA GTT CGA CTT CTT GTC

1666 GAA GCT GCC GCC GTT CCT CGA GGA GAT CTG GGA CGT GGC GGA CGT
CTT CGA CGG CGG CAA GGA GCT CCT CTA GAC CCT GCA CCG CCT GCA

1711 GGC GAC GAC GGC GAC GCC GGT GGC GGC GGC GGC GCC TCT
CCG CTG CTG CCG CTG CCG CCA CCG CCG CCT CCG CCG CGG CGG AGA

Fig.2 iv.

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1756 AGC CCC CGC CCC GCC CGC CGC GCC GCC CGC CAC CGT CTA GCG CGC
TCG GGG GCG GCG GGG CGG CGG GCG CGG CGG GTG GCA GAT CGC GCG

1801 CTC AGG AGA GAA CGC TCA TAG ACT GGC TAG TTT TAG TGA AGT GCA
GAG TCC TCT CTT GCG AGT ATC TGA CCG ATC AAA ATC ACT TCA CGT

1846 CGG ACA CTG ACG TCG ACG TGA TCA ACC TAT TTA TAA GGA CTG CGA
GCC TGT GAC TGC AGC TGC ACT AGT TGG ATA AAT ATT CCT GAC GCT

1891 ATT TTA CCA CTT AAG AGG GCA CAC CCG TAC CCG ATT TCG TAC GG
TAA AAT GGT GAA TTC TCC CGT GTG GGC ATG GGC TAA AGC ATG CC
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Total number of bases is: 1934.

Fig.3.

The sequence shown below is that of pSK16.1

Sequence ID3

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | CGC | TGG | TAT | AAC | AAC | GGA | CCA | TTC | CAG | ACG | CTG | CGA | ATG | CTC | GAG |
| | GCG | ACC | ATA | TTG | TTG | CCT | GGT | AAG | GTC | TGC | GAC | GCT | TAC | GAG | CTC |
| 46 | GAG | AGC | TCG | TCT | GAG | GTG | ACG | TCG | TCT | TCA | GCA | CTG | GGC | CTG | CCG |
| | CTC | TCG | AGC | AGA | CTC | CAC | TGC | AGC | AGA | AGT | CGT | GAC | CCG | GAC | GGC |
| 91 | CCG | GCT | ATG | GTG | ATG | TCC | CCG | GAA | TCG | CTC | GCG | TCG | CCC | GAG | ATC |
| | GGC | CGA | TAC | CAC | TAC | AGG | GGC | CTT | AGC | GAG | CGC | AGC | GGG | CTC | TAG |
| 136 | GGC | GGC | CTG | GAG | CTG | TGG | GGC | TAC | GAC | GAT | GGC | ATC | ACT | TAC | AGC |
| | CCG | CCG | GAC | CTC | GAC | ACC | CCG | ATG | CTG | CTA | CCG | TAG | TGA | ATG | TCG |
| 181 | ATG | GCA | CAG | TCG | CTG | GGC | ACC | TGC | ACC | ATG | GAG | CAG | CAG | CAG | CCC |
| | TAC | CGT | GTC | AGC | GAC | CCG | TGG | ACG | TGG | TAC | CTC | GTC | GTC | GTC | GGG |

Fig.3 i.

226 CAG CCG CAG CAG CCG CAG CAG ACA CAA CCC CTA CCT TCC ATG
GTC GGC GTC GTC GGC GTC GTC TGT GGT GGG GAT GGA AGG TAC

271 CCG TTA CCA ATG CCA CCG ACA ACA CCC AAA TCA GAA AAC GAG TCA
GGC AAT GGT TAC GGT GGC TGT TGT GGT TTT AGT CTT TTG CTC AGT

316 ATG TCA TCA GGT CGT GAG GAA CTG TCT CCA GCT TCG AGT GTA AAC
TAC AGT AGT CCA GCA CTC CTT GAC AGA GGT CGA AGC TCA CAT TTG

361 GGC TGC AGC ACA GAT GGC GAG GCG AGG CCG CAG AAG AAA GGC CCA
CCG ACG TCG TGT CTA CCG CTC CGC TCC GCC GTC TTC TTT CCG GGT

406 GCG CCG AGG CAG CAA GAA GAG CTA TGT GTC TGC GGC GAC AGA
CGC GGC TCC GTC GTC CTT CTC GAT ACA GAA CAG ACG CCG CTG TCT

451 GCC TCC GGA TAT CAC TAC AAC GCG CTC ACA TGT GAA GGG TGT AAA
CGG AGG CCT ATA GTG ATG TTG CGC GAG TGT ACA CTT CCC ACA TTT

496 GGT TTC TTC AGG CCG AGT GTA ACC AAA AAT GCA GTG TAC ATA TGC

Fig.3 ii.

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CCA AAG AAG TCC GCC TCA CAT TGG TTT TTA CGT CAC ATG TAT ACG
541 AAA TTC GGC CAT GCT TGC GAA ATG GAT ATC TAT ATG CCG AGA AAA
TTT AAG CCG GTA CGA ACG CTT TAC CTA TAG ATA TAC GCC TCT TTT

586 TGT CAG GAG TGT CGG TTG AAG AAA TGT CTT GCG GTG GGC ATG AGG
ACA GTC CTC ACA GCC AAC TTC TTT ACA GAA CGC CAC CCG TAC TCC

631 CCC GAG TGC GTG GTG CCG GAG AAC CAG TGT GCA ATG AAA CGG AAA
GGG CTC ACG CAC CAC GGC CTC TTG GTC ACA CGT TAC TTT GCC TTT

676 GAG AAA AAG GCG CAG AGG GAA AAA GAC AAA TTG CCC GTC AGT ACG
CTC TTT TTC CGC GTC TCC CTT TTT CTG TTT AAC GGG CAG TCA TGC

721 ACG ACA GTA GAC GAT CAC ATG CCT CCC ATC ATG CAA TGT GAC CCT
TGC TGT CAT CTG CTA GTG TAC GGA GGG TAG TAC GTT ACA CTG GGA

766 CCG CCC CCA GAG GCC GCT AGA ATT CTG GAA TGT GTG CAG CAC GAG
GGC GGG GGT CTC CGG CGA TCT TAA GAC CTT ACA CAC GTC GTG CTC

811 GTG GTG CCA CGA TTC CTG AAT GAG AAG CTA ATG GAA CAG AAC AGA
CAC CAC GGT GCT AAG GAC TTA CTC TTC GAT TAC CTT GTC TTG TCT

856 TTG AAG AAC GTG CCC CCC CTC ACT GCC AAT CAG AAG TCG TTG ATC
AAC TTC TTG CAC GCG GGG GAG TGA CGG TTA GTC TTC AGC AAC TAG

901 GCA AGG CTC GTG TGG TAC CAG GAA GGC TAT GAA CAA CCT TCC GAG
CGT TCC GAG CAC ACC ATG GTC CTT CCG ATA CTT GTT GGA AGG CTC

946 GAA GAC CTG AAG AGG GTT ACA CAG TCG GAC GAG GAC GAA GAC
CTT CTG GAC TTC TCC CAA TGT GTC AGC CTG CTC CTG CTT CTG

```

Fig.3 iii.

991 TCG GAT ATG CCG TTC CGT CAG ATT ACC GAG ATG ACG ATT CTC ACA
AGC CTA TAC GGC AAG GCA GTC TAA TGG CTC TAC TGC TAA GAG TGT

1036 GTG CAG CTC ATC GTA GAA TTC GCT AAG GGC CTC CCG GGC TTC GCC
CAC GTC GAG TAG CAT CTT AAG CGA TTC CCG GAG GGC CCG AAG CGG

1081 AAG ATC TCG CAG TCG GAC CAG ATC ACG TTA TTA AAG GCG TGC TCA
TTC TAG AGC GTC AGC CTG GTC TAG TGC AAT TTC CGC ACG AGT

1126 AGT GAG GTG ATG ATG CTC CGA GTG GCT CGG TAT GAC GCG GCC
TCA CTC CAC TAC TAC GAG GCT CAC CGA GCC ATA CTG CGC CGG

1171 ACC GAC AGC GTA CTG TTC GCG AAC AAC CAG GCG TAC ACT CGC GAC
TGG CTG TCG CAT GAC AAG CGC TTG TTC GTC CGC ATG TGA GCG CTG

1216 AAC TAC CGC AAG GCA GGC ATG GCG TAC GTC ATC GAG GAC CTG CTG
TTG ATG GCG TTC CGT CCG TAC CGC ATG CAG TAG CTC CTG GAC GAC

1261 CAC TTC TGT CGG TGC ATG TAC TCC ATG ATG ATG GAT AAC GTG CAT
GTG AAG ACA GCC ACG TAC ATG AGG TAC TAC TAC CTA TTG CAC GTA

1306 TAT GCG CTG CTT ACA GCC ATT GTC ATC TTC TCA GAC CGG CCC GGG
ATA CGC GAC GAA TGT CGG TAA CAG TAG AAG AGT CTG GCC GCG CCC

1351 CTT GAG CAA CCC CTG TTG GTG GAG GAC ATC CAG AGA TAT TAC CTG
GAA CTC GTT GGG GAC AAC CAC CTC CTG TAG GTC TCT ATA ATG GAC

1396 AAC ACG CTA CGG GTG TAC ATC CTG AAC CAG AAC AGC GCG TCG CCC
TTG TGC GAT GCC CAC ATG TAG GAC TTG GTC TTG TCG CGC AGC GGG

1441 CGC GGC GCC GTC ATC TTC GGC GAG ATC CTG GGC ATA CTG ACG GAG

Fig.3 iv.

| | | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | GCG | CCG | CCG | CAG | TAG | AAG | CCG | CTC | TAG | GAC | CCG | TAT | GAC | TGC | CTC |
| 1486 | ATC | CGC | ACG | CTG | GGC | ATG | CAG | AAC | TCC | AAC | ATG | TGC | ATC | TCC | CTC |
| | TAG | GCG | TGC | GAC | CCG | TAC | GTC | TTG | AGG | TTG | TAC | ACG | TAG | AGG | GAG |
| 1531 | AAG | CTG | AAG | AAC | AGG | AAG | CTG | CCG | CCG | TTC | CTC | GAG | GAG | ATC | TGG |
| | TTC | GAC | TTC | TTG | TCC | TTC | GAC | GGC | GGC | AAG | GAG | CTC | CTC | TAG | ACC |
| 1576 | GAC | GTG | GCG | GAC | GTG | GCG | ACG | ACG | GCG | ACG | CCG | GTG | GCG | GCG | GAG |
| | CTG | CAC | CGC | CTG | CAC | CGC | TGC | TGC | CGC | TGC | GGC | CAC | CGC | CGC | CTC |
| 1621 | GCG | CCG | GCG | CCT | CTA | GCC | CCC | GCC | CCG | CCC | GCC | CGG | CCG | CCC | GCC |
| | CGC | GGC | CGC | GGA | GAT | CGG | GGG | CGG | GGC | GGG | CGG | GCC | GGC | GGG | CGG |
| 1666 | ACC | GTC | TAG | CGC | GCC | TCA | GGA | GAG | AAC | GCT | CAT | AGA | CTG | GCT | AGT |
| | TGG | CAG | ATC | GCG | CGG | AGT | CCT | CTC | TTG | CGA | GTA | TCT | GAC | CGA | TCA |
| 1711 | TTT | AGT | GAA | GTG | CAC | GGA | CAC | TGA | CGT | CGA | CGT | GAT | CAA | CCT | ATT |
| | AAA | TCA | CTT | CAC | GTG | CCT | GTG | ACT | GCA | GCT | GCA | CTA | GTT | GGA | TAA |
| 1756 | TAT | AAG | GAC | TGC | GAA | TTT | TAC | CAC | TTA | AGA | GGG | CAC | ACC | CGT | ACC |
| | ATA | TTC | CTG | ACG | CTT | AAA | ATG | GTG | AAT | TCT | CCC | GTG | TGG | GCA | TGG |
| 1801 | CGA | TTT | CGT | ACG | TAT | TCG | GTG | ACC | GAC | GAC | GAT | GCA | GAG | CGT | GTG |
| | GCT | AAA | GCA | TGC | ATA | AGC | CAC | TGG | CTG | CTG | CTA | CGT | CTC | GCA | CAC |
| 1846 | TAA | TGT | GAA | TAT | ATG | TGT | TGT | TGA | ACG | ATT | TGG | AGA | ATA | TAT | ATT |
| | ATT | ACA | CTT | ATA | TAC | ACA | ACA | ACT | TGC | TAA | ACC | TCT | TAT | ATA | TAA |
| 1891 | GGT | GTT | GCT | GTT | CGG | GCC | CGC | ACG | CCG | TCG | CCG | GTC | GGC | GGC | GAT |
| | CCA | CAA | CGA | CAA | GCC | CGG | GCG | TGC | GGC | AGC | GGC | CAG | CCG | CCG | CTA |

Fig.3 v.

1936 CGC GGC GCC CGC GGC TTC AGT TTT ATT TCG TTT ACG ACT GAG TTG
GCG CCG CGG GCG CCG AAG TCA AAA TAA AGC AAA TGC TGA CTC AAC

1981 GTC ACT CGG ATA CGA CTG TAT GAT AAG ACT TCG TTC GAT AAG TAC
CAG TGA GCC TAT GCT GAC ATA CTA TTC TGA AGC AAG CTA TTC ATG

2026 ACC TAC TAA ATT ACA CAT ACG TAC GTA GCT TAC GAG AGT TAT TAG
TGG ATG ATT TAA TGT GTA TGC ATG CAT CGA ATG CTC TCA ATA ATC

2071 AGA CAA AGA ATA TAA GAA GAA GAT GTT TCT ATT GGG TGA AAA GTT
TCT GTT TCT TAT TAT ATT CTT CTT CTA CAA AGA TAA CCC ACT TTT CAA

2116 GAT AGT TAT GTT TAT TTA CCA AAA TTA ACA ATA ATA CGT TGA TTA
CTA TCA ATA CAA ATA AAT GGT TTT AAT TGT TAT TAT GCA ACT AAT

2161 ACC TTT CGA GTA TAA TAT TGT GAT GAG TCG TCC GCT GTC CAC GTC
TGG AAA GCT CAT ATT ATA ACA CTA CTC AGC AGG CGA CAG GTG CAG

2206 GCC GTC ACA TGT TTG TTT CTG ATG CAC ACG TGA GGN GCG TTA TCG
CGG CAG TGT ACA AAC AAA GAC TAC GTG TGC ACT CCN CGC AAT AGC

2251 TGT TTC ATG GTT CCA TCG TCC TGT GCC CGC GAC CCT CGA CTA AAT
ACA AAG TAC CAA GGT AGC AGG ACA CGG GCG CTG GGA GCT GAT TTA

2296 GAG TAA TTT AAT TTA TTG CTG TGA TTA CAT TTT AAT GTG TTG ATT
CTC ATT AAA TTA AAT AAC GAC ACT AAT AAT GTA AAA TTA CAC AAC TAA

2341 ATC TAC CAT AGG GTG ATA TAA GTG TGT CTT ATT ACA ATA CAA AGT
TAG ATG GTA TCC CAC TAT ATT CAC ACA GAA TAA TGT TAT GTT TCA

2386 GTG TGT CGT CGA TAG CTT CCA CAC GAG CAA GCC TTT TGT TTA AGT

Fig.3 vi. CAC ACA GCA GCT ATC GAA GGT GTG CTC GTT CGG AAA ACA AAT TCA
 2431 GAT TTA CTG ACA TGG ACA CTC GAC CCG GAA CTT C
 CTA AAT GAC TGT ACC TGT GAG CTG GGC CTT GAA G

Total number of bases is: 2464.

Fig.4.

Sequence ID 4

| | | | | | |
|---|-----|-----|-----|-----|-----|
| 10 | 20 | 30 | 40 | 50 | 60 |
| | | | | | |
| ACTCGCGTGCTCTTCTCACCCGTGTTGCTCGGATTGTGTGTACTAGAAAAAGTTGTTCGCC | | | | | |
| 70 | 80 | 90 | 100 | 110 | 120 |
| | | | | | |
| GCTCGAACGAGACTTCCGAGTCCCTATTGGATTGCCACGAAAGTCGAGACAGTGGATAGCGA | | | | | |
| 130 | 140 | 150 | 160 | 170 | 180 |
| | | | | | |
| TTCCGGTTTCGTTTGAACGTTGCCGTAGACGAGTGTGTGCATGTCCATGAGTCGCCGTTTAGAT | | | | | |

Fig.4 i.

190 | 200 | 210 | 220 | 230 | 240 |
AGTTTAGTCCGAGGAAAGTGAAGTGAAGCCCTTCTCGGAGGATGTCCCTCGGGCGCTC
M S L G A
250 | 260 | 270 | 280 | 290 | 300 |
GTGGATACCGGAGGTGTGACACGCTCGCCGACATGAGACGCCCGCTGGTATAACAACGGAC
R G Y R R C D T L A D M R R R W Y N N G
310 | 320 | 330 | 340 | 350 | 360 |
CATTCCAGACGCTGCCGAATGCTCGAGGAGAGCTCGTCTGAGGTACGTCGTCCTTCAGCAC
P F Q T L R M L E E S S S E V T S S S A
370 | 380 | 390 | 400 | 410 | 420 |
TGGGCTGCCGCGGCTATGGTGATGTCCCCGGAATCGCTCGCGTCGCCCGAGATCGGGCG
L G L P P A M V M S P E S L A S P E I G

Fig.4 ii.

430 | 440 | 450 | 460 | 470 | 480 |
GCCTGGAGCTGTGGGGCTACGACGATGGCATCACTTACAGCATGGCACAGTCGCTGGGCA
G L E L W G Y D D G I T Y S M A Q S L G

490 | 500 | 510 | 520 | 530 | 540 |
CCTGCACCATGGAGCAGCAGCAGCCCCAGCCGCAGCAGCAGCCGCAGCAGACACAACCCC
T C T M E Q Q Q P Q Q P Q Q Q T Q P

550 | 560 | 570 | 580 | 590 | 600 |
TACCTTCCATGCCGTTACCAATGCCACCGACAACACCCAAATCAGAAAACGAGTCAATGT
L P S M P L P M P P T T P K S E N E S M

610 | 620 | 630 | 640 | 650 | 660 |
CATCAGGTCGTGAGGAACGTCTCCAGCTTCGAGTGTAACGGCTGCAGCACAGATGGCG
S S G R E E L S P A S S V N G C S T D G

670 | 680 | 690 | 700 | 710 | 720 |
AGGCGAGGCGCAGAGAAAGGCCCGCCGAGCGCAGCAAGAGAGCTATGTCTTGTCT
E A R R Q K K G P A P R Q Q E E L C L V

Fig.4 iii.

730 | 740 | 750 | 760 | 770 | 780 |
 GCGGCACAGAGCCTCCGGATATCACTACAACGGCTCACATGTGAAGGTGTAAGGTT
 C G D R A S G Y H Y N A L T C E G C K G
 790 | 800 | 810 | 820 | 830 | 840 |
 TCTTCAGGCGAGTGTAACCAAAATGCAGTGACATATGCAAATTCGGCCATGCTTCCG
 F F R R S V T K N A V Y I C K F G H A C
 850 | 860 | 870 | 880 | 890 | 900 |
 AAATGGATATCTATGCGGAGAAAATGTCAGGAGTGTGCGTTGAAGAAATGCTCTTCCG
 E M D I Y M R R K C Q E C R L K K C L A
 910 | 920 | 930 | 940 | 950 | 960 |
 TGGGCATGAGGCCCGAGTGCCTGGTCCGGAGAACCAAGTGTGCAATGAAACGGAAAGAGA
 V G M R P E C V V P E N Q C A M K R K E
 970 | 980 | 990 | 1000 | 1010 | 1020 |
 AAAAGGCCAGAGGAAAAGACAAATTGCCCGTCAGTACGACGACAGTAGACGATCACA
 K K A Q R E K D K L P V S T T V D D H

Fig.4 iv.

1030 1040 1050 1060 1070 1080
| | | | |
TGCCTCCCATGCAATGTGACCCCTCCGCCCCAGAGCCGCTAGAAATTCTGGAATGTG
M P P I M Q C D P P P E A A R I L E C
1090 1100 1110 1120 1130 1140
| | | | |
TGCAGCACGAGGTGTGCCACGATTCTGTAATGAGAAGCTAATGGAACAGAACAGATTGA
V Q H E V V P R F L N E K L M E Q N R L
1150 1160 1170 1180 1190 1200
| | | | |
AGAACGTGCCCCCTCACTGCCAATCAGAAGTCGTTGATCGCAAGGCTCGTGTGTACC
K N V P P L T A N Q K S L I A R L V W Y
1210 1220 1230 1240 1250 1260
| | | | |
AGGAAGGCTATGAACAACCTTCCGAGGAAGACCTGAAGAGGGTTACACAGTCGGACGAGG
Q E G Y E Q P S E E D L K R V T Q S D E

Fig.4 v.

1270 1280 1290 1300 1310 1320
ACGACGAAGACTCGGATATGCCGTTCCGTCAGATTACCGAGATGACGATTCTCACAGTGC
D D E D S D M P F R Q I T E M T I L T V
1330 1340 1350 1360 1370 1380
AGCTCATCGTAGAATTCGCTAAGGGCCTCCCGGGCTTCGCCAAGATCTCGCAGTCGGACC
Q L I V E F A K G L P G F A K I S Q S D
1390 1400 1410 1420 1430 1440
AGATCACGTTATTAAAGGCGTGCTCAAGTGAGGTGATGATGCTCCGAGTGGCTCGGCGGT
Q I T L L K A C S S E V M M L R V A R R
1450 1460 1470 1480 1490 1500
ATGACGGGCCACCGACAGCGTACTGTTCGCCGAACAACCGCGGTACACTCGCGACAAC
Y D A A T D S V L F A N N Q A Y T R D N

Fig.4 vi.

1510 1520 1530 1540 1550 1560
ACGCAAGGCAGGCATGGCGTACGTTCATCGAGGACCTGCTGCACTTCTGTCTCGGTGCATGT
Y R K A G M A Y V I E D L L H F C R C M
1570 1580 1590 1600 1610 1620
ACTCCATGATGGATAACGTGCATTATGCGCTGCTTACAGCCATTGTCATCTTCTCAG
Y S M M D N V H Y A L L T A I V I F S
1630 1640 1650 1660 1670 1680
ACCGCCCGGCTTGAGCAACCCCTGTTGTGGAGGAGATCCAGAGATATTACCTGAACA
D R P G L E Q P L L V E E I Q R Y Y L N
1690 1700 1710 1720 1730 1740
CGCTACGGGTGTACATCCTGAACCAGAACAGCGCGTCCCGCCCGCGCGGTCACTCTTCG
T L R V Y I L N Q N S A S P R G A V I F

Fig.4 vii.

1750 1760 1770 1780 1790 1800
GCGAGATCCTGGGCATACTGACGGAGATCCGCACGCTGGGCATGCAGAACTCCAACATGT
G E I L G I L T E I R T L G M Q N S N M
1810 1820 1830 1840 1850 1860
GCATCTCCCTCAAGCTGAAGAACAGGAAGCTGCCGCCGTTCTCTCAGGAGATCTGGGACG
C I S L K L K N R K L P P F L E E I W D
1870 1880 1890 1900 1910 1920
TGGCGGACGTGGCGACGACGGCGACGCCGGTGGCGGGGAGCGCGCGCCTCTAGCCCC
V A D V A T T A T P V A A E A P A P L A
1930 1940 1950 1960 1970 1980
CCGCCCCCGCCCCGCGCGCCGCCACCGTCTAGCGCGCCTCAGGAGAGAACGCTCATA
P A P P A R P P A T V -
1990 2000 2010 2020 2030 2040
GACTGGCTAGTTTGTAGTGAAGTGACGGACACTGACGCTCGACGTGATCAACCTATTATA

Fig.4 viii.

2050 | 2060 | 2070 | 2080 | 2090 | 2100 |
AGGACTGCGAATTTTACCACCTTAAGAGGGCACACCCGTACCCGATTTCGTACGTATTCGG
2110 | 2120 | 2130 | 2140 | 2150 | 2160 |
TGACCGACGACGATGCAGAGCGTGTGTAATGTGAATATATGTGTGTTGTTGAACGATTTCGA
2170 | 2180 | 2190 | 2200 | 2210 | 2220 |
GAATATATATTGGTGTGCTGTTTCGGGCCCCGCACGCCGTCGCCGGTCGGCGGCGATCCGG
2230 | 2240 | 2250 | 2260 | 2270 | 2280 |
GCGCCCGCGGCTTCAGTTTATTTTCGTTTACGACTGAGTTGGTCACTCGGATACGACTGT
2290 | 2300 | 2310 | 2320 | 2330 | 2340 |
ATGATAAGACTTCGTTCCGATAAAGTACACCTACTACTAAATTACACATACGTACGTAGCTTACG
2350 | 2360 | 2370 | 2380 | 2390 | 2400 |
AGAGTTATTAGAGACAAAGAAATATAAGAGAGATGTTTCTATTGGGTGAAAAGTTGATA

Fig.4 ix.

2410 | 2420 | 2430 | 2440 | 2450 | 2460 |
GTTATGTTTATTACCAAAATTAACAATAATACGTTGATTAAACCTTTCGAGTATAATATT

2470 | 2480 | 2490 | 2500 | 2510 | 2520 |
GTGATGAGTCGTCGCTGTCCACGTCGCGGTCAACATGTTTGTTCGTGATGCACACGTGAG

2530 | 2540 | 2550 | 2560 | 2570 | 2580 |
GNGCGTTATCGTGTTCATGGTTCATCGTCCTGTGCCCGCGACCCCTCGACTAAATGAGT

2590 | 2600 | 2610 | 2620 | 2630 | 2640 |
AATTAAATTTATGCTGTGATTACATTTTAAATGTGTGATTATCTACCATAGGGTGATAT

2650 | 2660 | 2670 | 2680 | 2690 | 2700 |
AAGTGTGCTTATTACAATACAAAGTGTGTGTCGTCGATAGCTTCCACACGAGCAAGCCT

2710 | 2720 | 2730 | 2740 |
TTTGTTTAAAGTGATTACTGACATGGACACTCGACCCCGGAACCTTC

Fig.5.

Sequence I.D. 5

| | | | |
|-------|---|-----|--|
| BmECR | MRVENVDNVS | 10 | |
| MsECR | ----- | | |
| HvECR | M----- | 1 | |
| CtECR | ----- | | |
| AaECR | ----- | | |
| DmECR | ----- | | |
| BmECR | FALNGRADEWCMSVETRLDSLVRKSEVKAYVGGCPVITDAGAYDALFD | 60 | |
| MsECR | ----- | | |
| HvECR | -SLGARGYRRC-----DTLAD | 16 | |
| CtECR | ----- | | |
| AaECR | ----- | | |
| DmECR | ----- | | |
| BmECR | M-RRRWSNNGGFP-LRMLEESSEVTSSA-LGLPPAMVMSPELASPEY | 107 | |
| MsECR | M-RRRWSNNGCFP-LRMFEESSEVTSSA-FGMPAAMVMSPELASPEY | 47 | |
| HvECR | M-RRRWYNNGGFQTLRMLEESSEVTSSA-LGLPPAMVMSPELASPEI | 64 | |
| CtECR | M-K-----TENLIVTT-VKVEPLNYASQSF | 23 | |
| AaECR | MMKRRWSNNGGFTALRMLDDSSSEVTSSAAL----GMTMSPNSLGSPNY | 46 | |
| DmECR | M-KRRWSNNGGF--MRLPEESSEVTSSNGLVLPsgvnmSPSSLDSDHY | 47 | |
| | * * | | |

Fig.5 i.

| | | |
|-------|---|-----|
| BmECR | GALELW-----SY----- | 114 |
| MseCR | GGLELW-----SY----- | 55 |
| HvECR | GGLELW-----GY----- | 72 |
| CtECR | GDNNI-----YGGAT----- | 33 |
| AaECR | DELELW-SSYEDNAYNGHSV--LSNGNNN-----LGCGA- | 78 |
| DmECR | CDNDKWLCGNESGSGNGHGLSQQQQSVITLAMHGCSSTLPAQTIIIP | 97 |

| | | |
|-------|--|-----|
| BmECR | -----DDGITY | 121 |
| MseCR | -----DETMN | 61 |
| HvECR | -----DDGIT- | 77 |
| CtECR | -----KKQRLSEDETMNH | 46 |
| AaECR | -----ANLLMNGIVGNNNL-----NGMMN | 98 |
| DmECR | INGNANGGSTNGQYVPGATNLGALANGMLNGFGNGMQQQIQNGHGLIN | 147 |

...

| | | |
|-------|--|-----|
| BmECR | NTAQSLLGACNMQQQLQP-----QQHPAPPTLPTMP---- | 154 |
| MseCR | YPAQSLLGACNAPQQQQQ-----QQQPSAQPLPSMP---- | 94 |
| HvECR | YSMAQSLGTCIMEQQQP-----QQPQQTQPLPSMP---- | 114 |
| CtECR | NQTNMNLSSNMNHTIS-----GFSSPDVNYEAYSPNSKL-----DDGN | 86 |
| AaECR | MASQAVQANANSIQHIVGN-----LINGVNPNTLIPPLPS---- | 134 |
| DmECR | STTPSTPTTPLHLQQNLGGAGGGIGGMGILHHANGTPNGLIGVVGGGG | 197 |

| | | |
|-------|---|-----|
| BmECR | -----LPMPPPTPKSENESSMGREELSPASSINGCSADA--D | 190 |
| MseCR | -----LPMPPPTPKSENESSMGREELSPASSINGCSTDG--E | 130 |
| HvECR | -----LPMPPPTPKSENESSMGREELSPASSVNGCSTDG--E | 146 |
| CtECR | MSVHMGDG-----LDG-----K | 98 |
| AaECR | -----IIQNTLMNTPRSESVNSISSGREDLSPSSSLNGYT--DGSD | 173 |
| DmECR | VGLGVGGGVGGLGMQHTPRSDSVNSISSGRDDLSPSSSLNGYSANESCD | 247 |

.. *

BmECR
MsECR
HvECR
CtECR
AaECR
DmECR

ARRQKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV
 PRRQKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV
 ARRQKKGPAPRQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV
 KSSSKKGPVPRQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV
 AKKQKKGPTPRQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKNAV
 AKKSKKGPAPRVQEEELCLVCGDRASGYHYNALTCEGCKGFFRRSVTKSAV

[illegible]

YICKFGHACEMDMYMRKQCERLKKCLAVGMRPECVQEPS-KNKDRQR
YICKFGHACEMDMYMRKQCERLKKCLAVGMRPECVPESTCKNKRREK
YICKFGHACEMDIYMRKQCERLKKCLAVGMRPECVVPENQCAMKRKEK
YCKKFGECEMDMYMRKQCERLKKCLAVGMRPECVVPENQCAIKRKEK
YCKKFGHACEMDMYMRKQCERLKKCLAVGMRPECVVPENQCAIKRKEK
YCKKFGHACEMDMYMRKQCERLKKCLAVGMRPGCVVPGNQCAMKRREK
YCKKFGHACEMDMYMRKQCERLKKCLAVGMRPGCVVPGNQCAMKRREK

Y C C K F * G R A C E M D M I N R A C G L C A R A C E *

QKKDKGILLPVSTTV-----EDHMPPIMQC
EAQREKDKLPVSTTV-----DDHMPAIMQC
KAQREKDKLPVSTTV-----DDHMPPIMQC
KAQKEKDKVPGIVGSNTSSSLNQSLNNGSLKNLEISYREELLQQLMKC
KAQKEKDKVQTNAT-----VSTTNSTY-RS-----EILPILMKC
KAQKEKDKMTTSPSSQHGGNGSLASGGQDFVKK-----EILD-LMTC
KAQKEKDKMTTSPSSQHGGNGSLASGGQDFVKK-----EILD-LMTC * *

• • • • •

DPPPPEAARI-----HEVVPRYLSEKLM EQNRQKNIPPLSANQKSLIARL
 DPPPPEAARI-----HEVVPFRFLTEKLM EQNRRLKNVTPLSANQKSLIARL
 DPPPPEAARI-----HEVVPFRFLNEKLM EQNRRLKNVPPLTANQKSLIARL
 DPPPPEAARI-----PEKLLMENRAKGTPLTANQVAVIYKL
 DPPPPEAARI-----PEKLLQENRLRNIPLLTANQMAVIYKL
 DPPPPEAARI-----PDEILAKCQARNIPSLTYNQLAVITKL
 EPPQHATIPLL-----* * * * *

[illegible]

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•

•
•

✱
✱

BmECR
MsECR
HvECR
CtECR
AaECR
DmECR

BmECR
MsECR
HvECR
CtECR
AaECR
DmECR

VWYQEGYEQPSDEDLKRVQTWQ-SDEEDEESDLPFRQITEMTILTVQLI
VWYQEGYEQPSEEDLKRVQTWQLEEEEEETDMPFRQITEMTILTVQLI
VWYQEGYEQPSEEDLKRVQTQ---DEDESDMPFRQITEMTILTVQLI
VWYQEGYEQPSEEDLKRVQTQ---DEDESDMPFRQITEMTILTVQLI
IWYQDGYEQPSEEDLKRITE--LEEEEDQHEANFRYTEVTILTVQLI
IWYQDGYEQPSEEDLKRMIG--SPNEEDQHDVHFRHITEITILTVQLI
IWYQDGYEQPSEEDLRRIM-S--QPDENESQTDVSFRHITEITILTVQLI
IWYQDGYEQPSEEDLRRIM-S--QPDENESQTDVSFRHITEITILTVQLI

[illegible]

BmEcr
MsEcr
HvEcr
CtEcr
AaEcr
DmEcr

KAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHFALLTAIVIFSDDRP
 QAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDDRP
 QAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALLTAIVIFSDDRP
 QAYTRDNYRQAGMEETIDLLHFCRQMYALSIDNVETALLTAIVIFSDDRP
 TAYTKQTYQLAGMEETIDLLHFCRQMFSLTVDNVVEYALLTAIVIFSDDRP
 RSYTRDSYRMAGMADTIEDLLHFCRQMFSLTVDNVVEYALLTAIVIFSDDRP
 RSYTRDSYKMGAGMADNIEDLLHFCRQMFMSKVDNVVEYALLTAIVIFSDDRP

BmECR
MsECR
HvECR
CtECR
AaECR
DmECR

GLEQPSLVEEIQRYYLNTLRIYIINQNSASSRCAVIYGRILSVLTELRTL
GLEQPLLVEEIQRYYLKTLRVYILNQHSAPRCVLFCKILGVLTELRTL
GLEQPLLVEEIQRYYLNTLRVYILNQNSAPRGAVIFGEILGILTEIRTL
GLEQPLLVEEIQRYYLNTLRVYILNQNSAPRGAVIFGEILGILTELRTM
GLEKAEMVDIIQSYTETLKVYIVRDHGGESRCSVQFAKLLGILTELRTL
GLEQAELVEHIQSYVIDTLRIYILNRHAGDPKCSVIFAKLLSILTELRTL
GLEKAQQLVEAIQSYVIDTLRITILNRHCGDSMSLVFYAKLLSILTELRTL

BmECR
MsECR
HvECR
CtECR
AaECR
DmECR

Fig.5 iv.

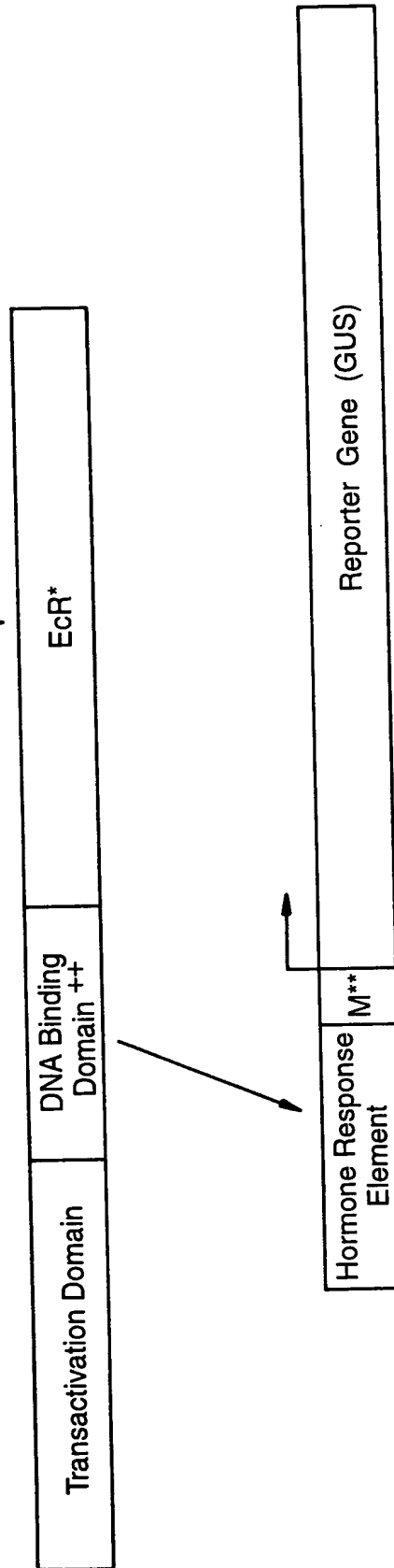
| | | |
|-------|--|-----|
| BmECR | GTQNSNMCISLKLKNRKLPPFLEEIWDVAEVARR----- | 593 |
| MseCR | GTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTT----- | 535 |
| HvECR | GMQNSNMCISLKLKKRKLPPFLEEIWDVADVATT----- | 552 |
| CtECR | GNLSEMCFSLKLNRNKLPRFLEEVDVGDVNNQTTATTNTENIVRERIN | 534 |
| AaECR | GNQSEMCFSLKLKNRKLPRFLEEIWDVDQDIPPSMQAQMHSHTQSSS--- | 590 |
| DmECR | GNQNAEMCFSLKLKNRKLPKFLEEIWDVHAIPPSVQSHLQITQEEDERLE | 674 |
| | * * * * * * * * * * | |
| BmECR | ----- | 593 |
| MseCR | ----- | 535 |
| HvECR | ----- | 552 |
| CtECR | ----- | 536 |
| AaECR | RN----- | 632 |
| DmECR | -----SSSSSSSSNGSSNGSSNSNSQHGPHPHGQQ--LTPNQ | 724 |
| | RAERMRAVGGAITAGIDCDSASTSAAAAAQHPQPQPQPSSLTQND | |
| BmECR | -----HPTV-----LPTNPVVL----- | 606 |
| MseCR | -----QP--TPGVAAQVTPIVVDNPAAL----- | 556 |
| HvECR | -----ATPVAAEAPAPLAPAPPARPATV----- | 575 |
| CtECR | ----- | 536 |
| AaECR | QQHQQQ-----HSQLQQ-----V | 645 |
| DmECR | SQHQTQPQLQPQLPPQLQGQLQPQLQTLQTLQPIQPQPQLLPVSAPV | 774 |
| BmECR | ----- | 606 |
| MseCR | ----- | 556 |
| HvECR | ----- | 575 |
| CtECR | ----- | 536 |
| AaECR | HANGSGGGGNNSSSG----- | 663 |
| DmECR | PASVTAPGSLSAVSTSEYMGGSAAIGPITPATTSITAAVTASSTTSAPV | 824 |

Fig.5 v.

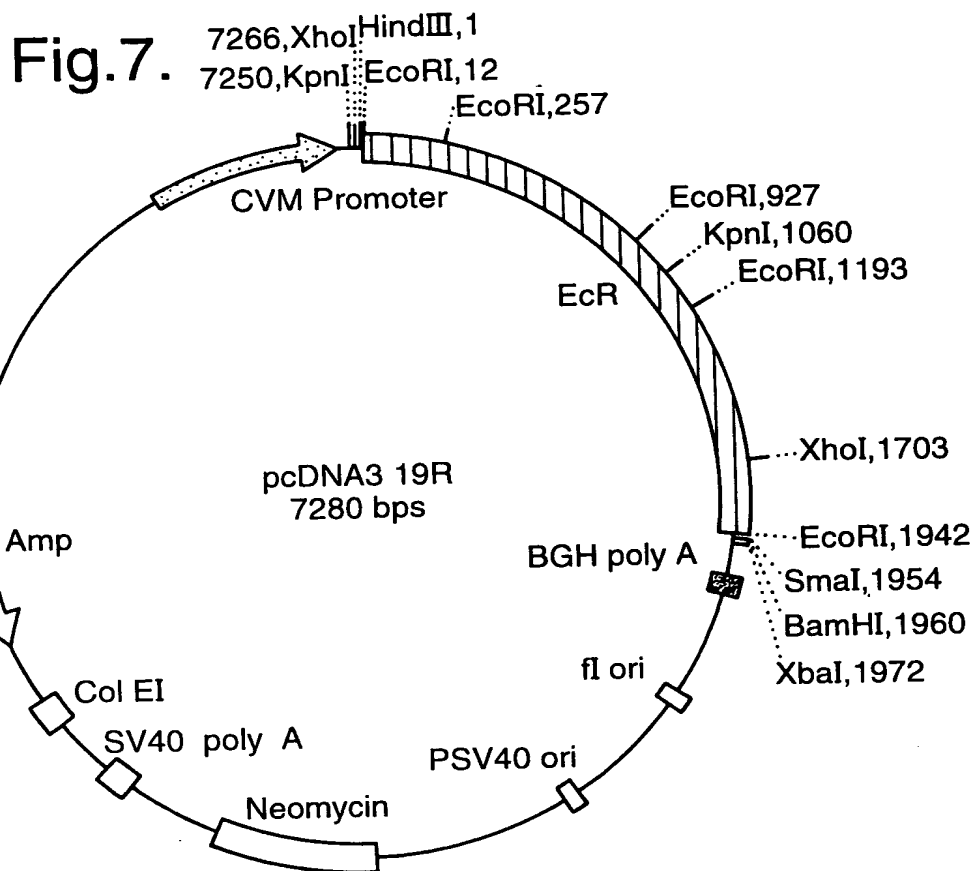
| | | |
|-------|--|-----|
| BmECR | ----- | 606 |
| MsECR | ----- | 556 |
| HvECR | ----- | 575 |
| CtECR | ----- | 536 |
| AaECR | -----GVVPGLGMLDQV----- | 675 |
| DmECR | PMGNGVGVGVGGNVSMYANAQTAMALMGVALHSHQQQLIGGVAVKSEH | 874 |

| | | |
|-------|------|-----|
| BmECR | --- | 606 |
| MsECR | --- | 556 |
| HvECR | --- | 575 |
| CtECR | --- | 536 |
| AaECR | --- | 675 |
| DmECR | STTA | 878 |

Fig.6. Chemical



- ++ Glucocorticoid receptor DNA binding and transactivation domains
- * Insect ecdysone ligand binding domain
- ** Minimal 35S CaMV promoter



Response Element for HecR → → → →

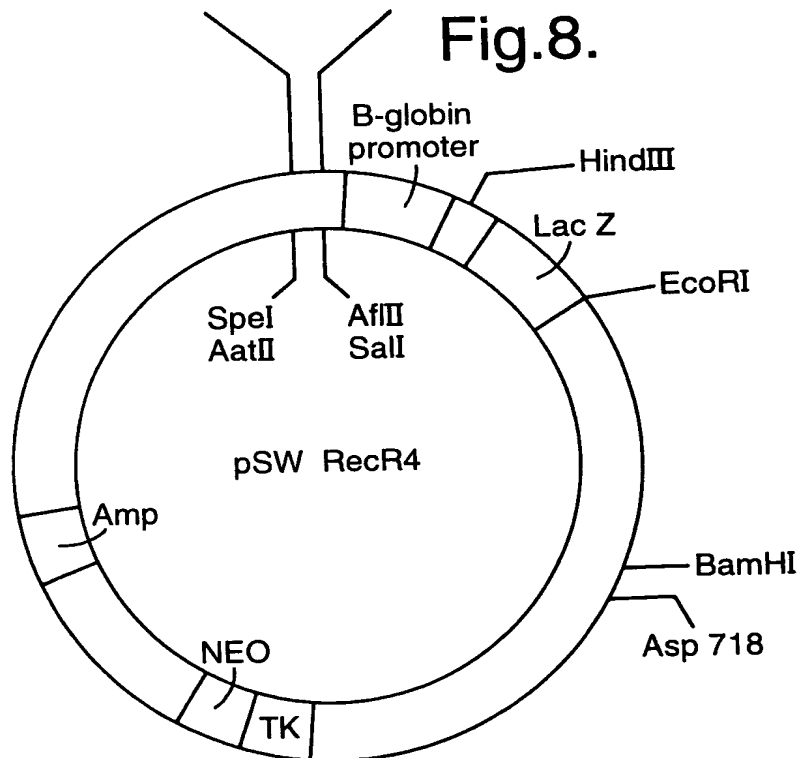


Fig.9.

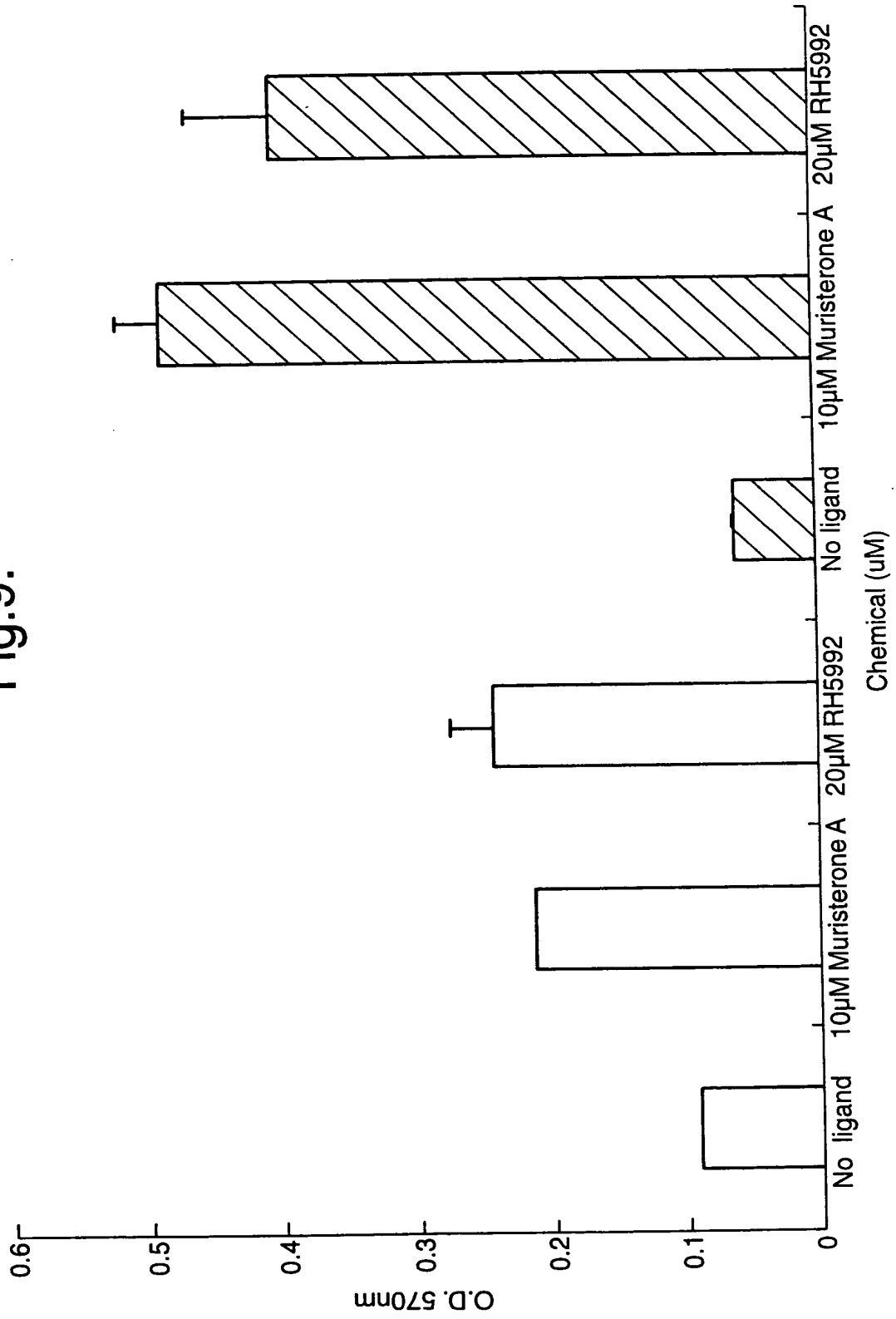


Fig.10.

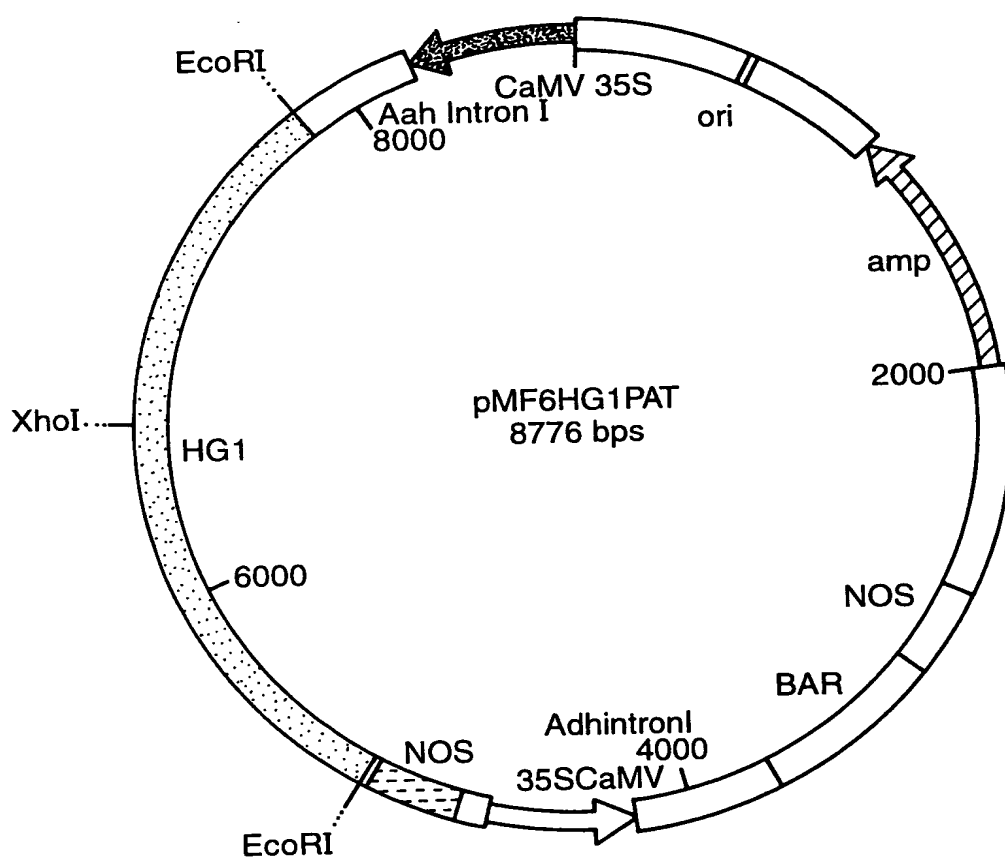


Fig.11.

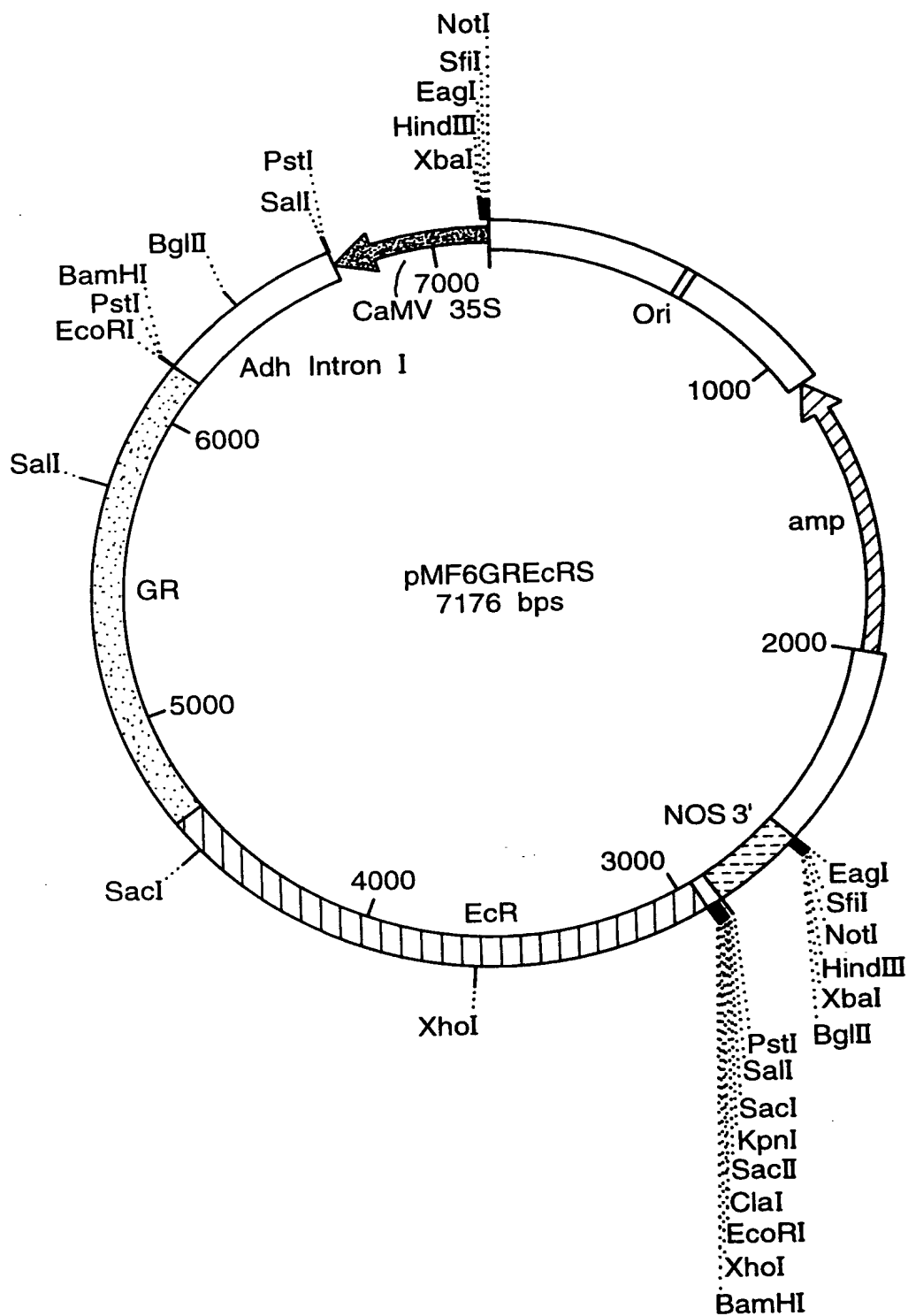


Fig.12.

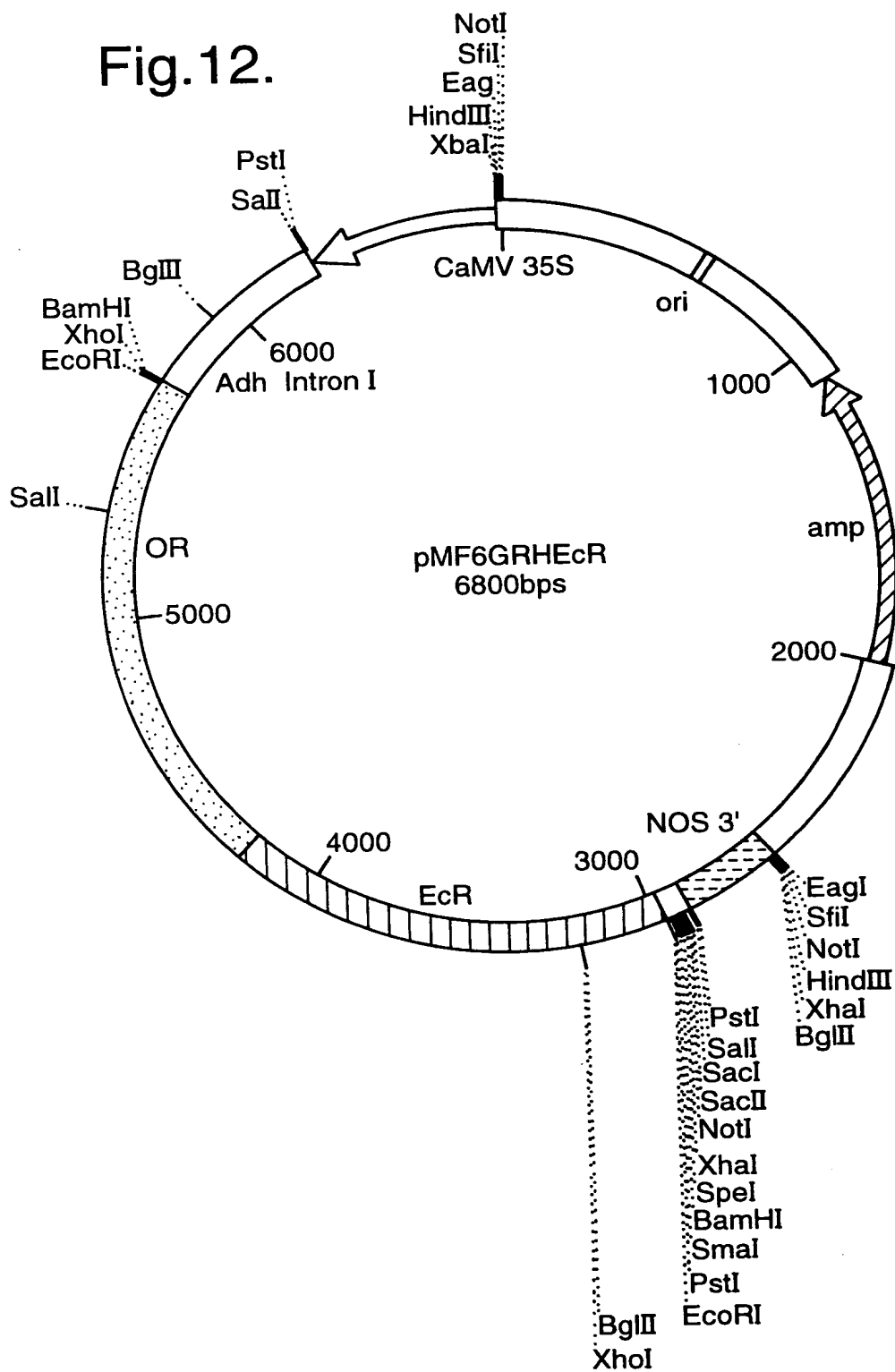


Fig.13.

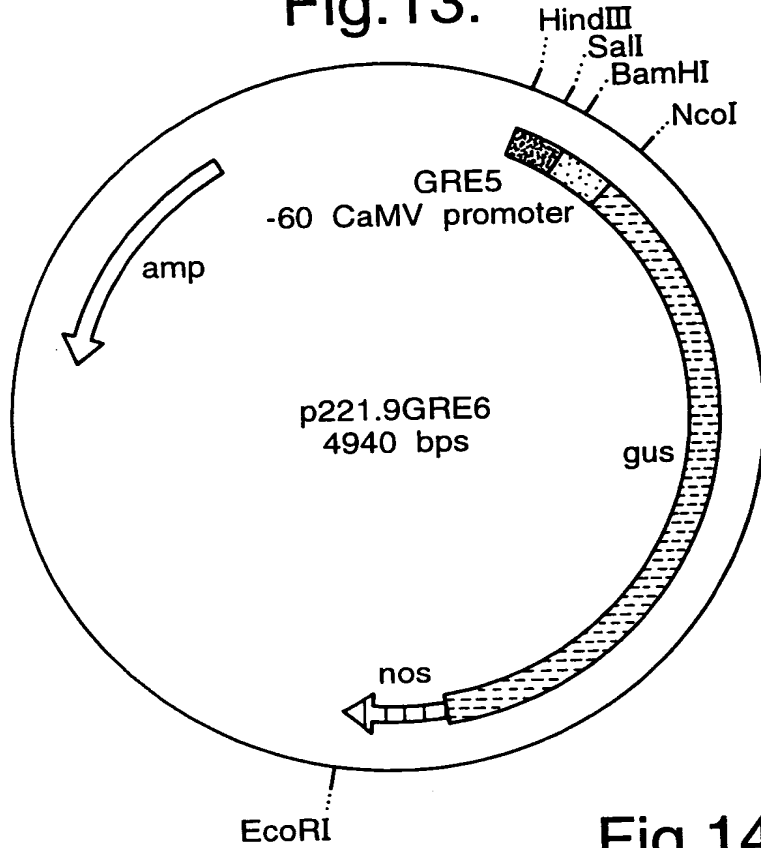


Fig.14.

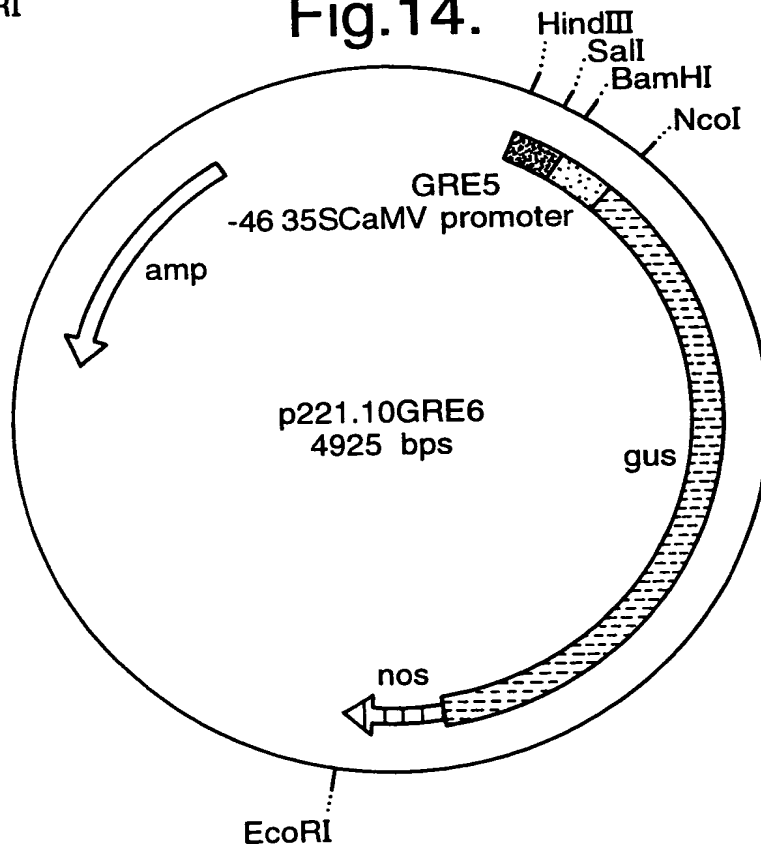


Fig.15.

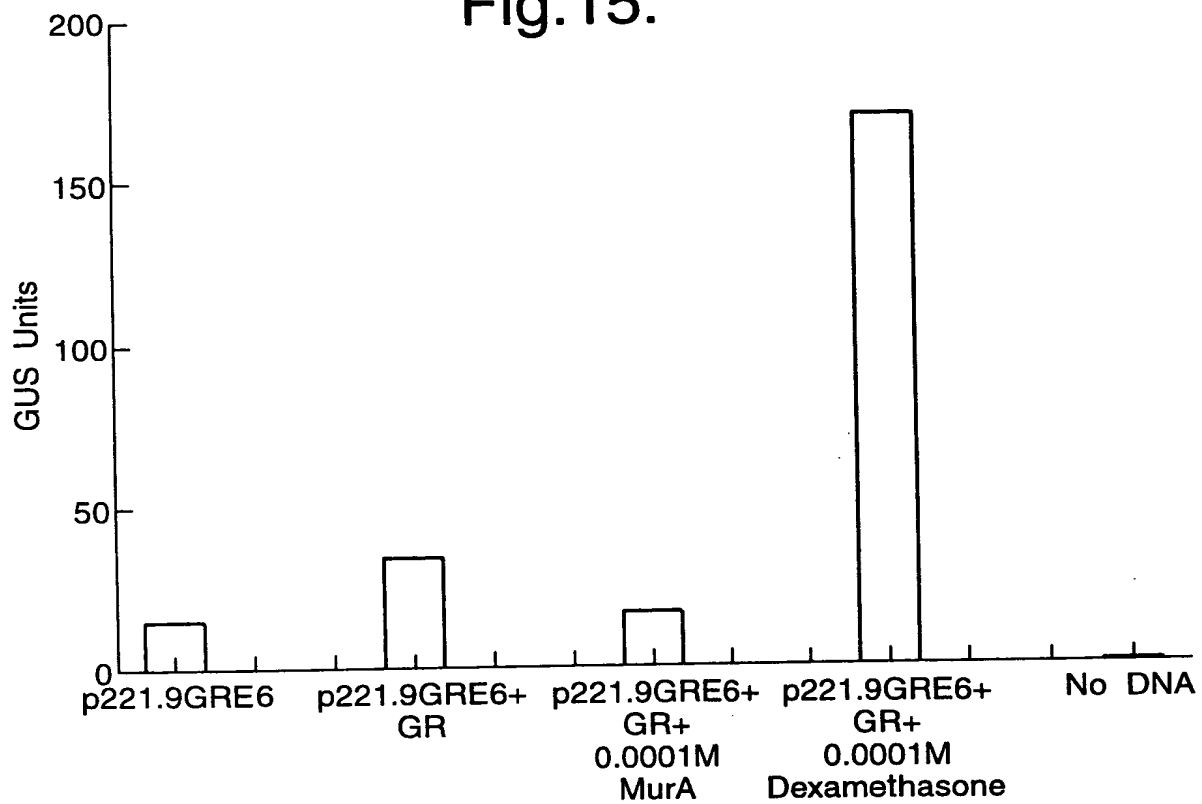


Fig.16.

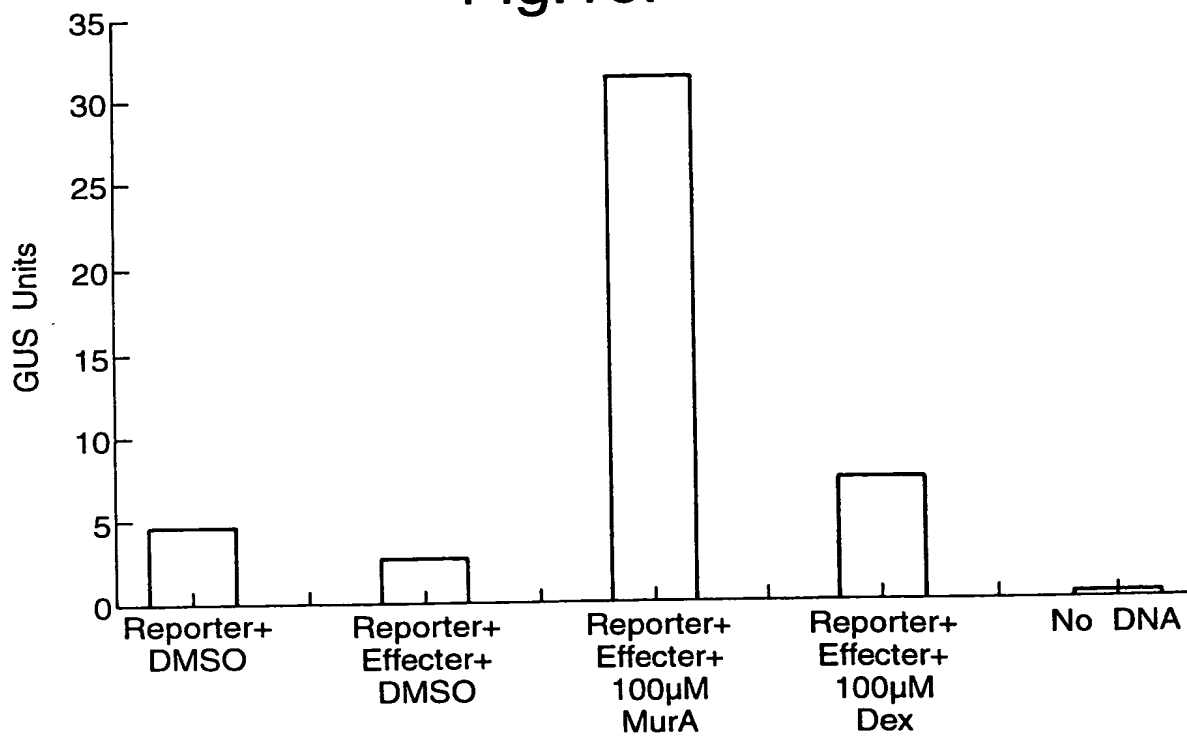


Fig.17.

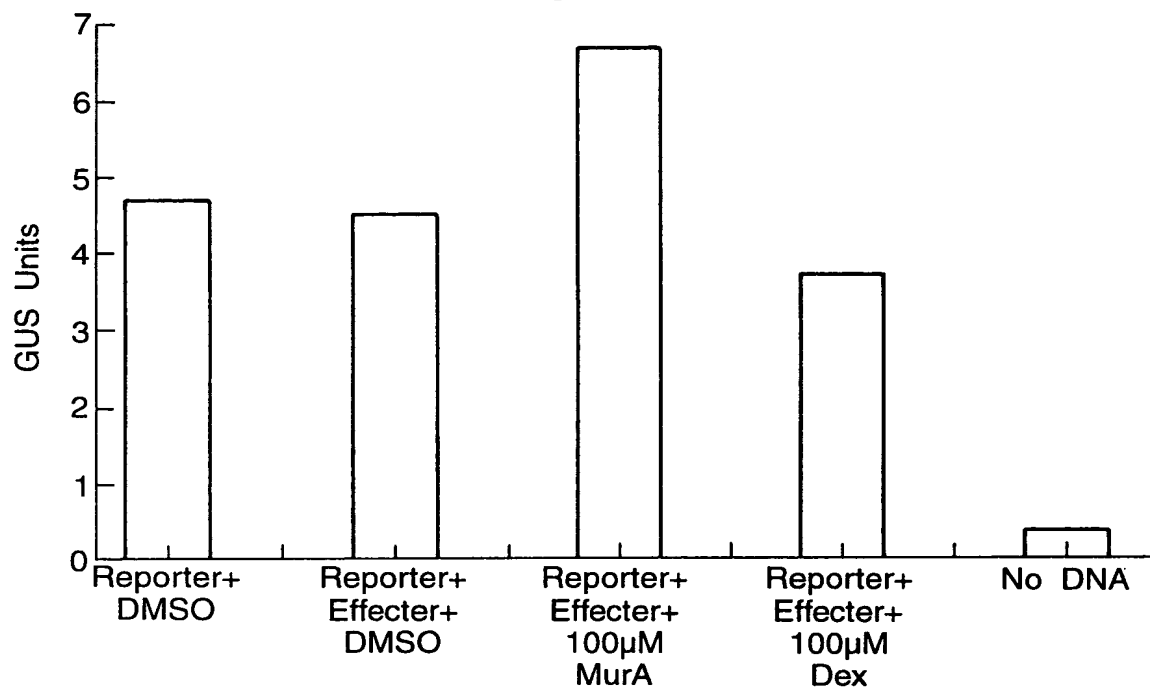


Fig.18.

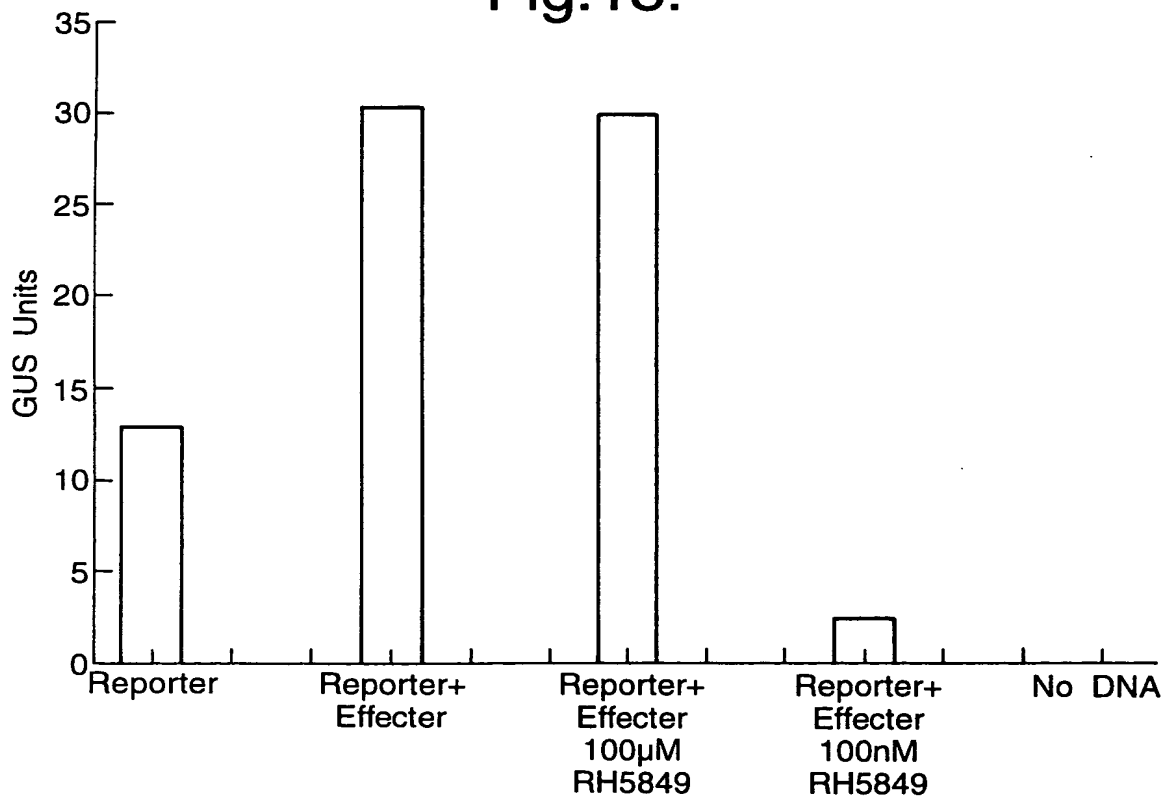


Fig.19.

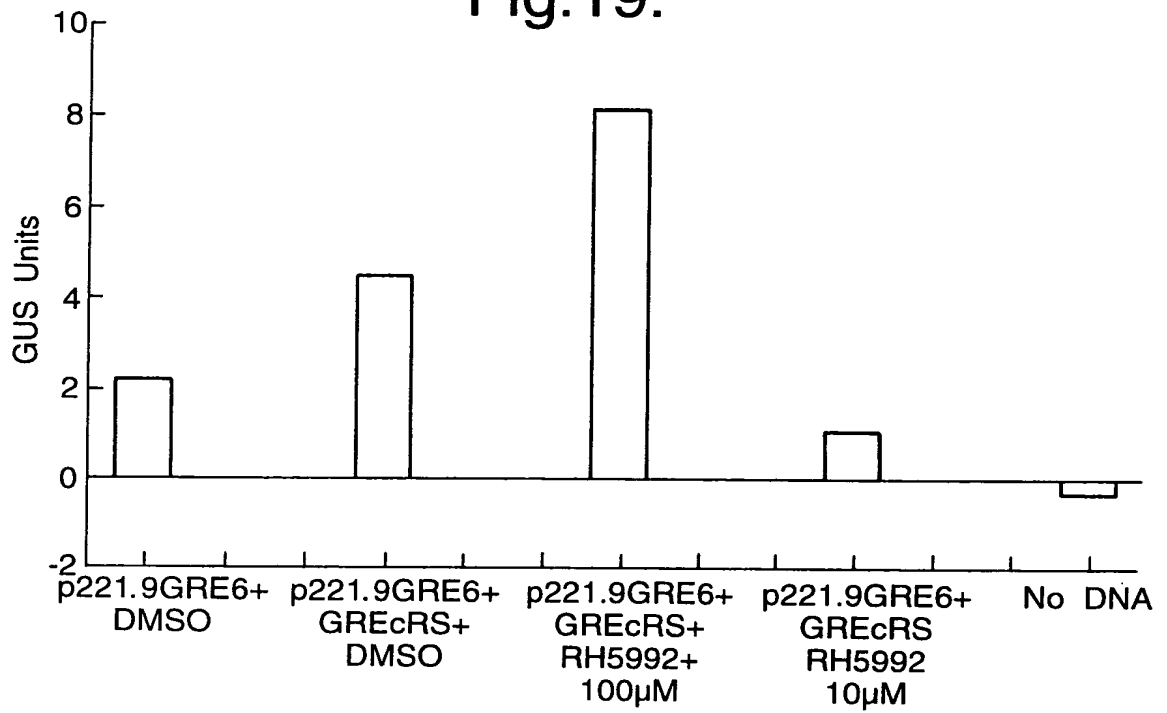


Fig.20.

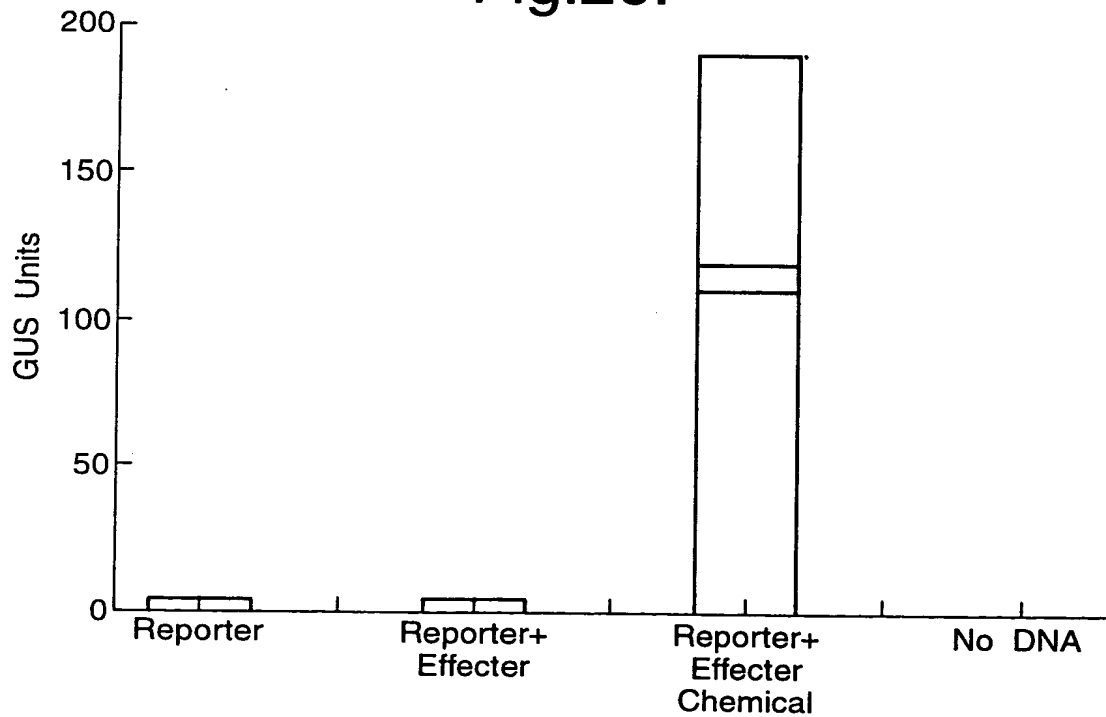


Fig.21.

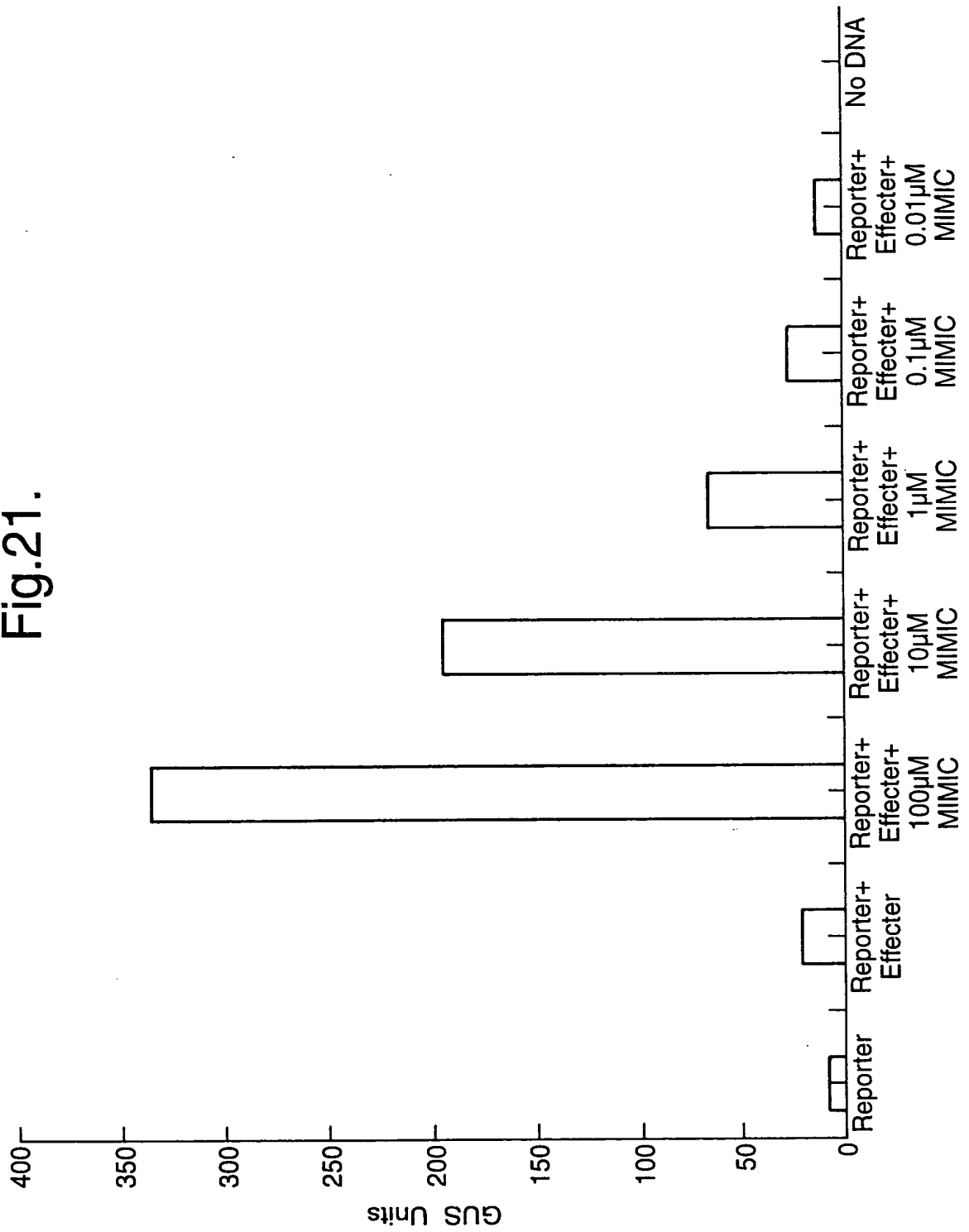


Fig.22.

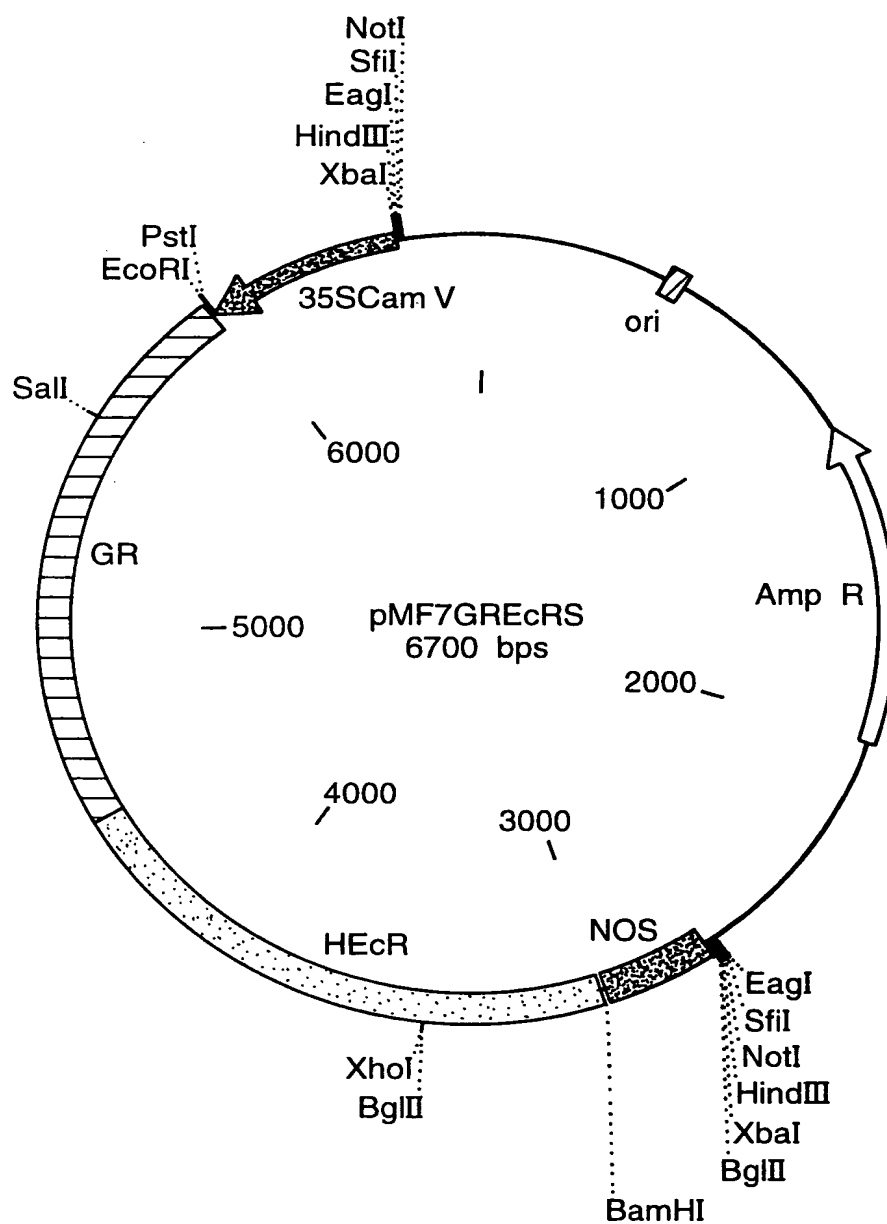


Fig.23.

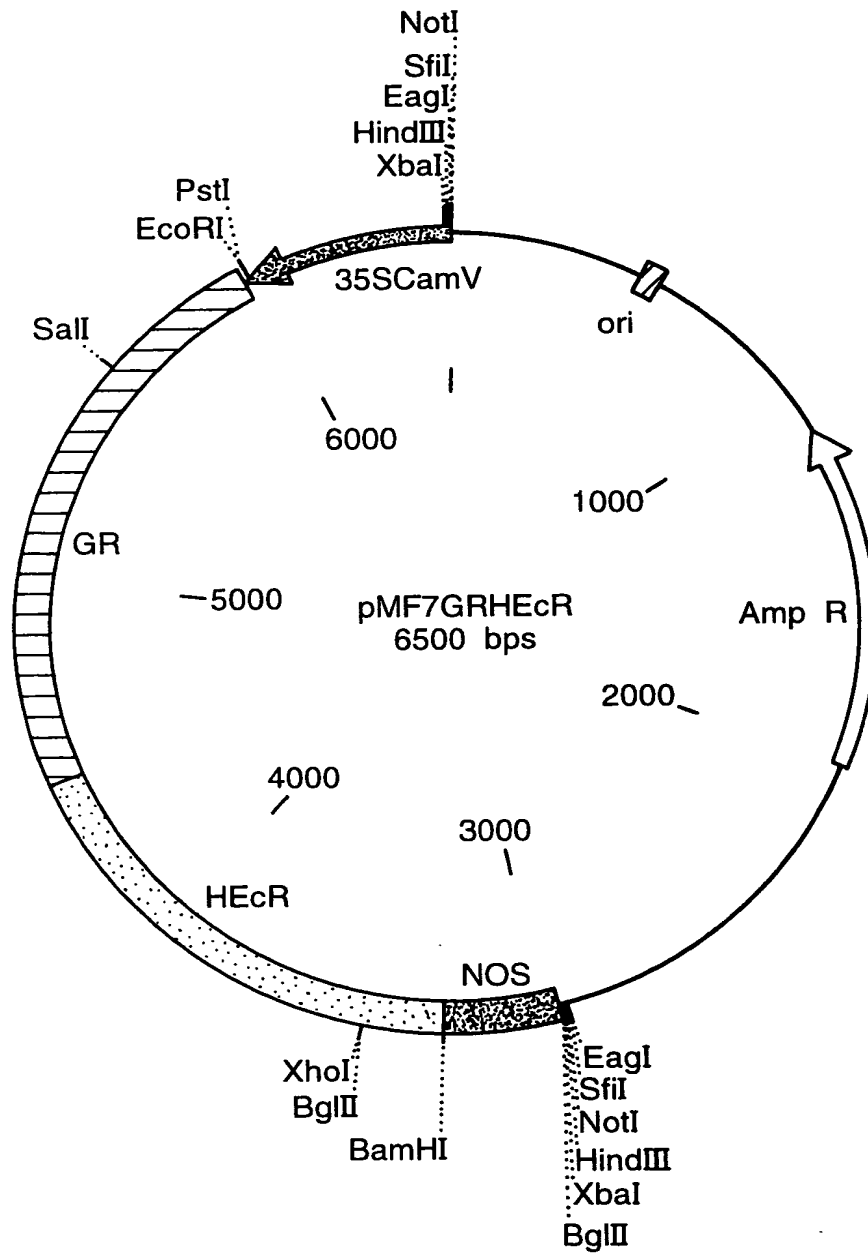


Fig.24.

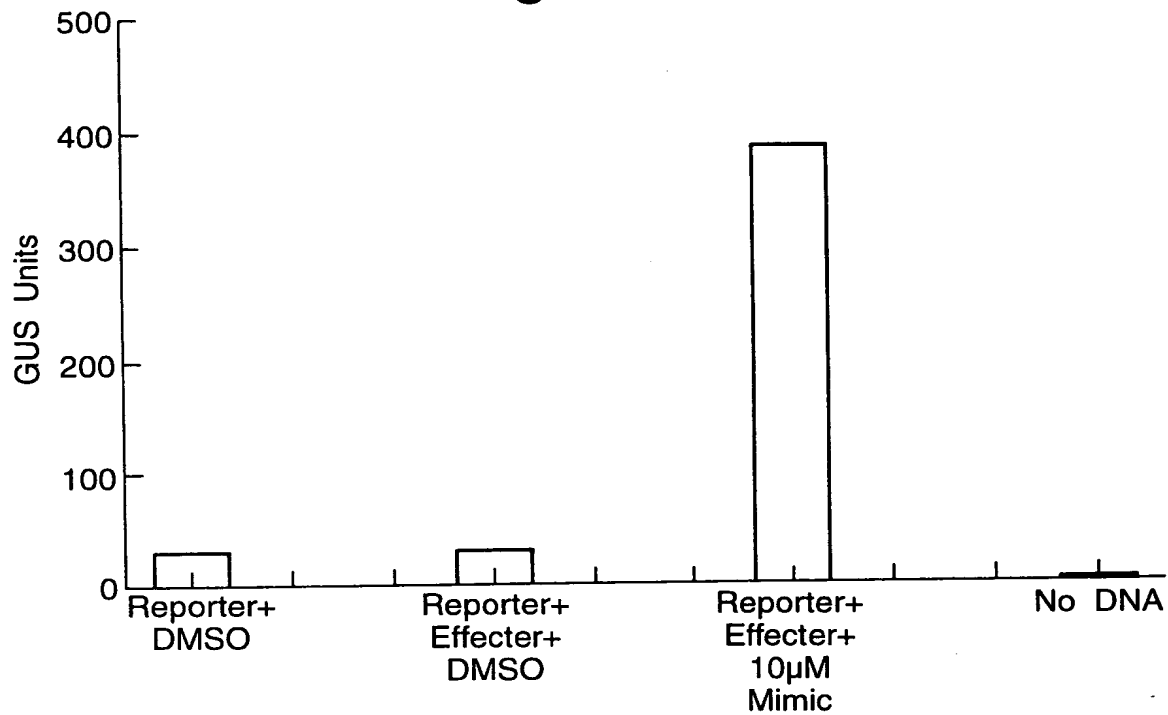


Fig.26.

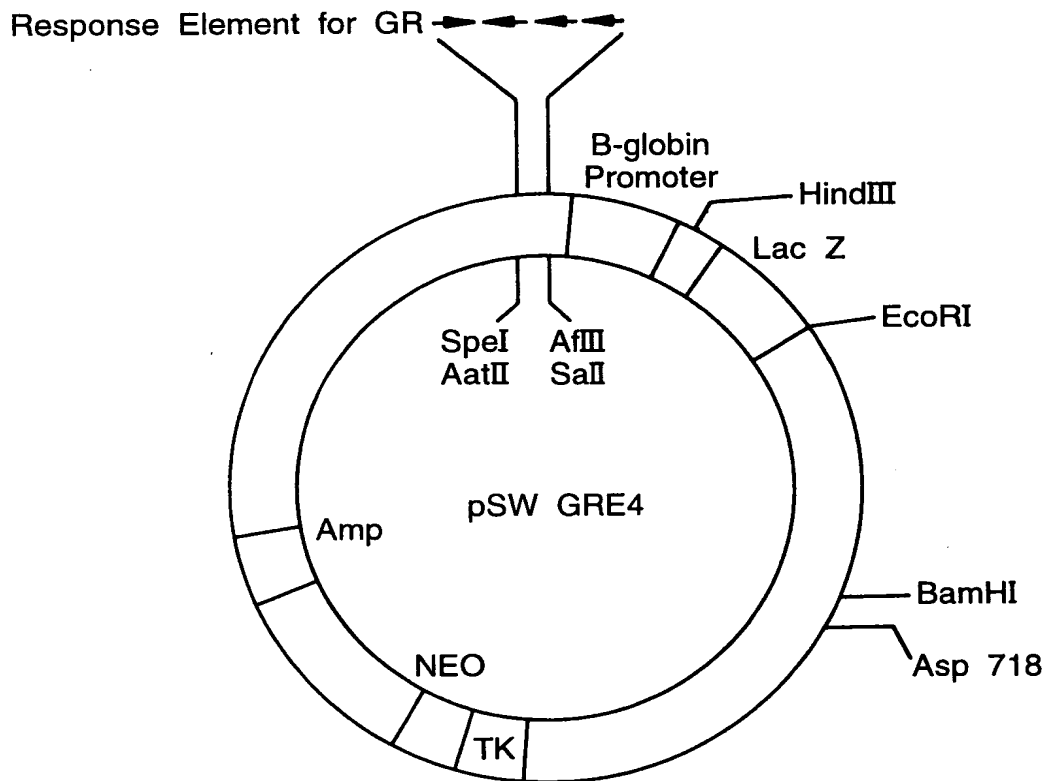


Fig.25.

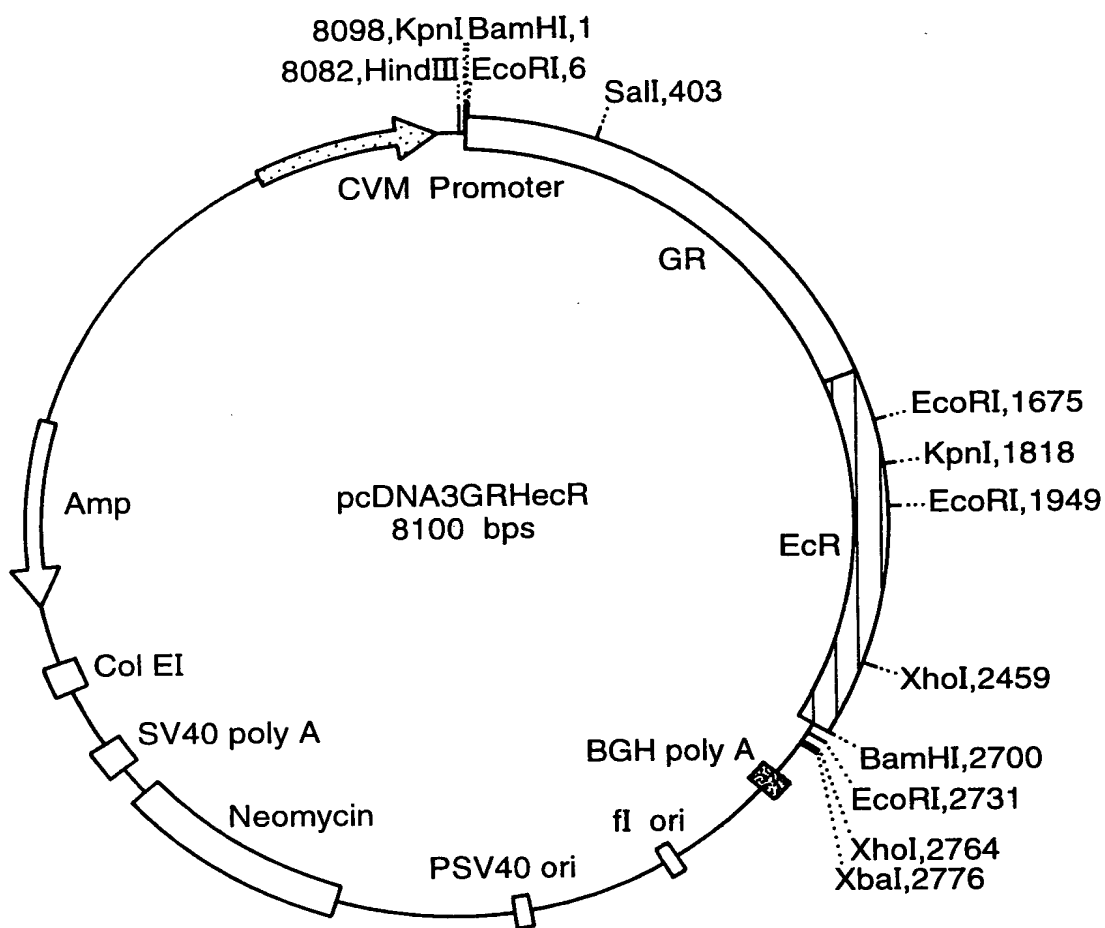


Fig.27.

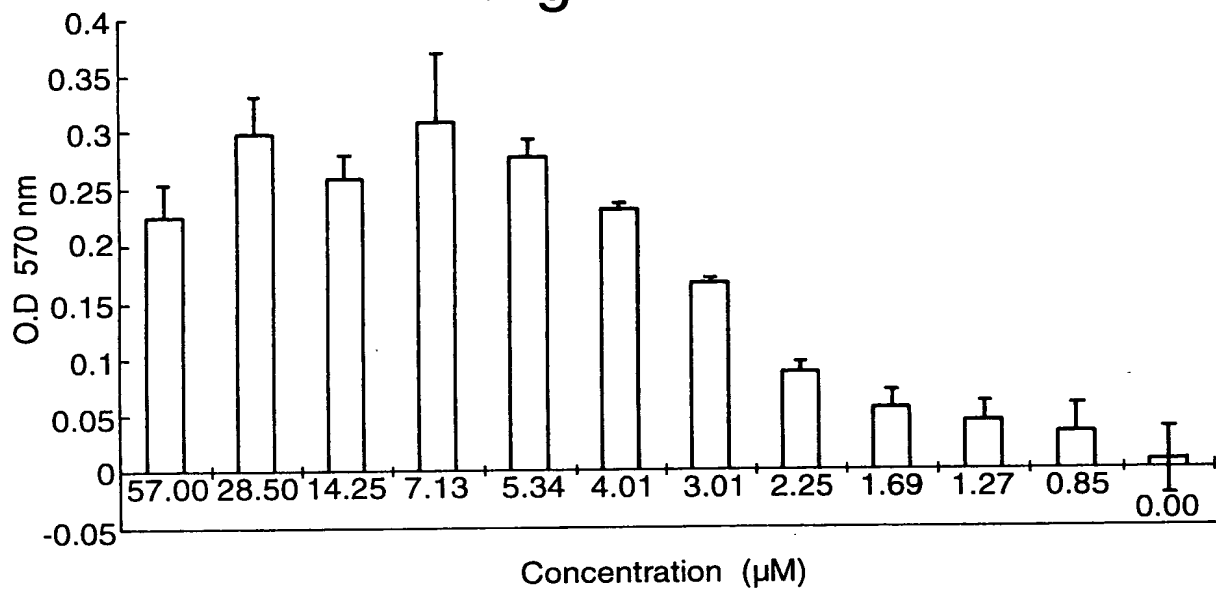


Fig.28.

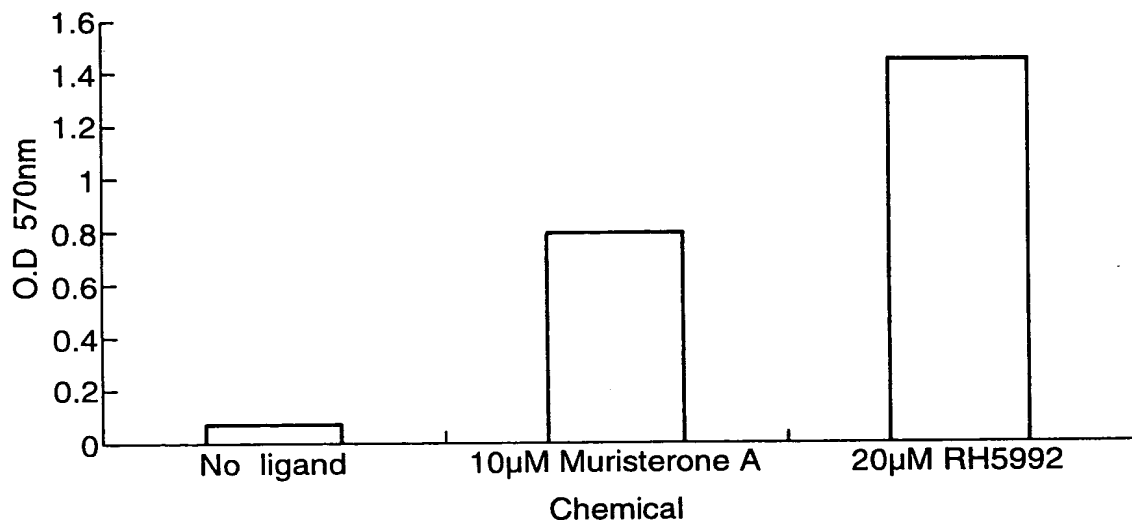


Fig.29.

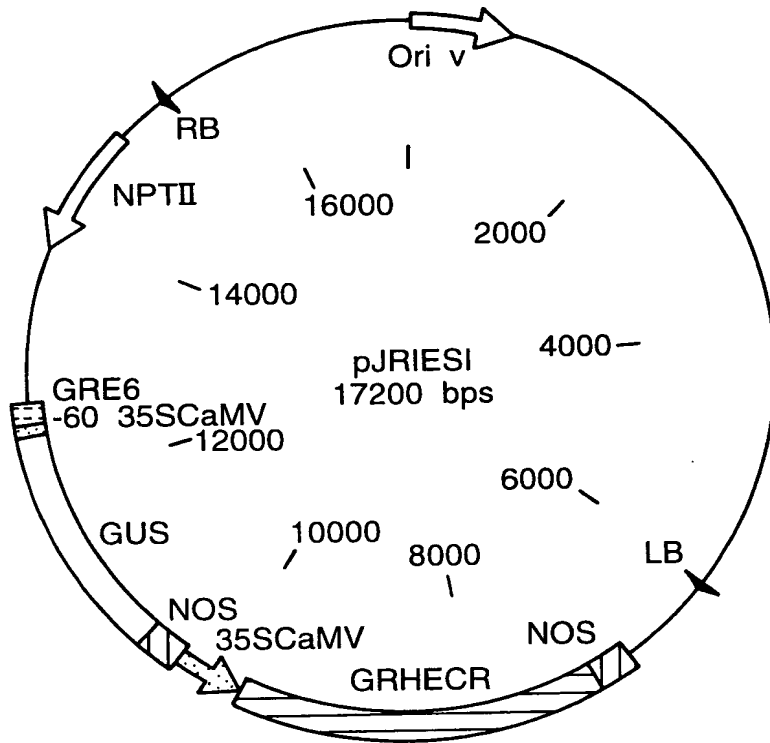


Fig.30.

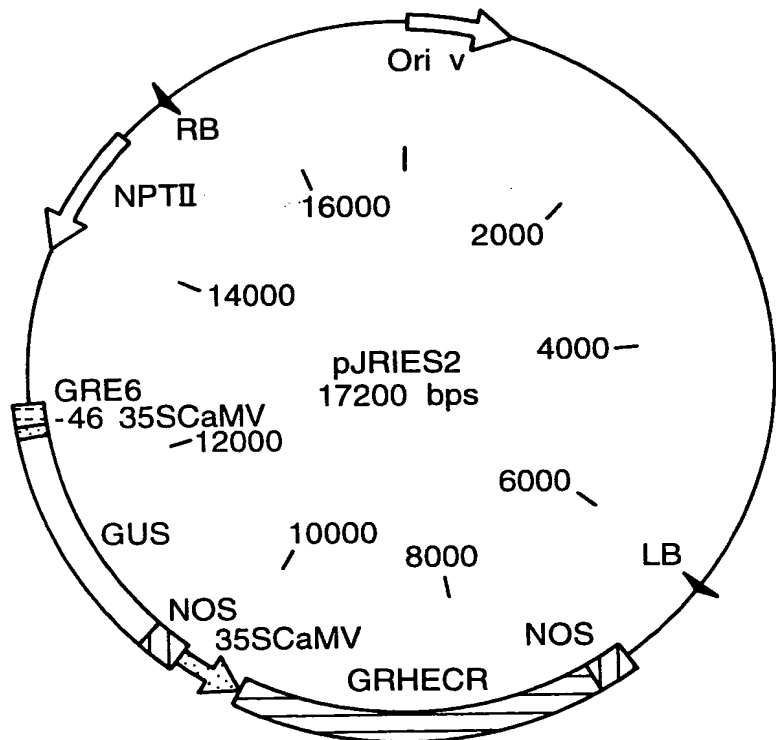


Fig.31.

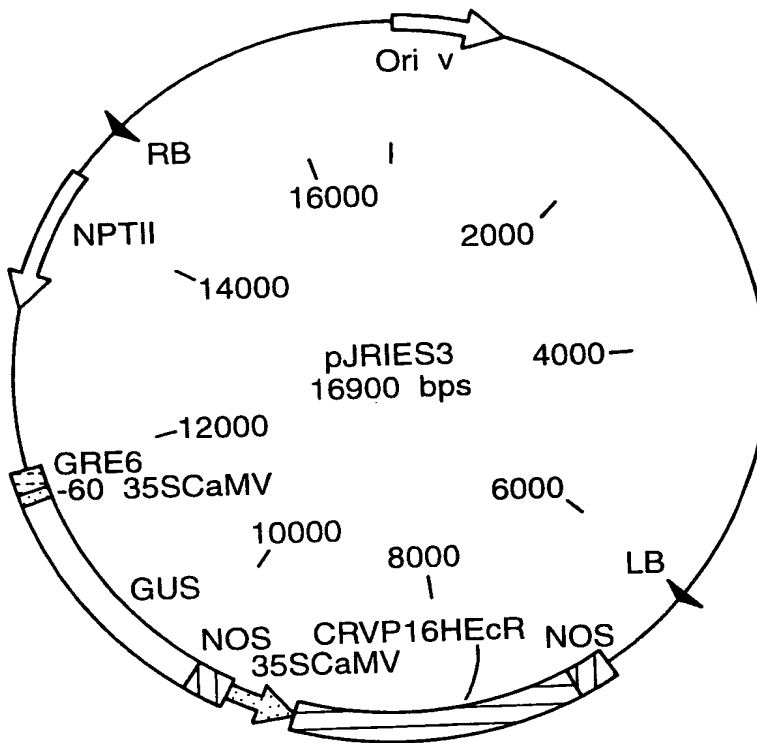


Fig.32.

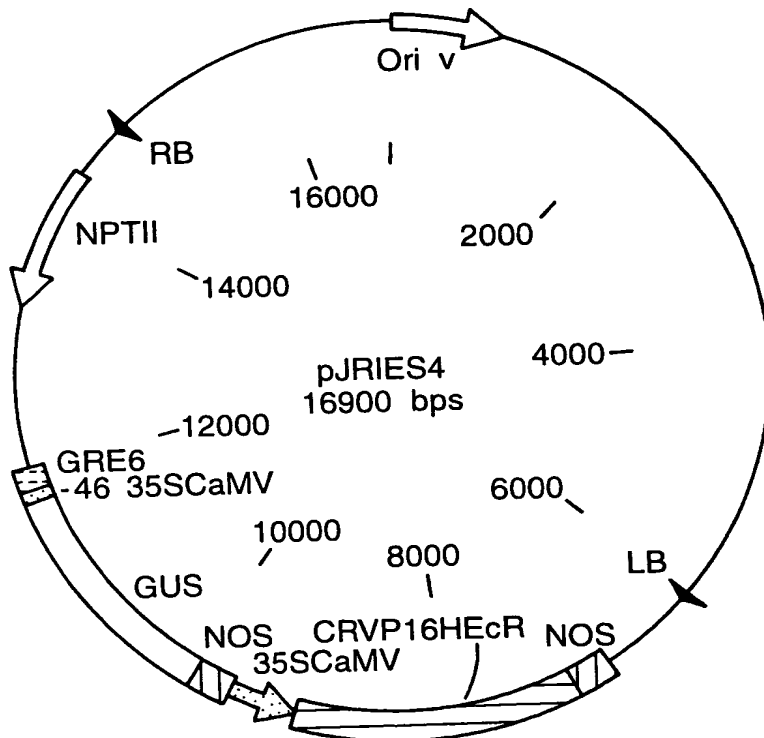


Fig.33.

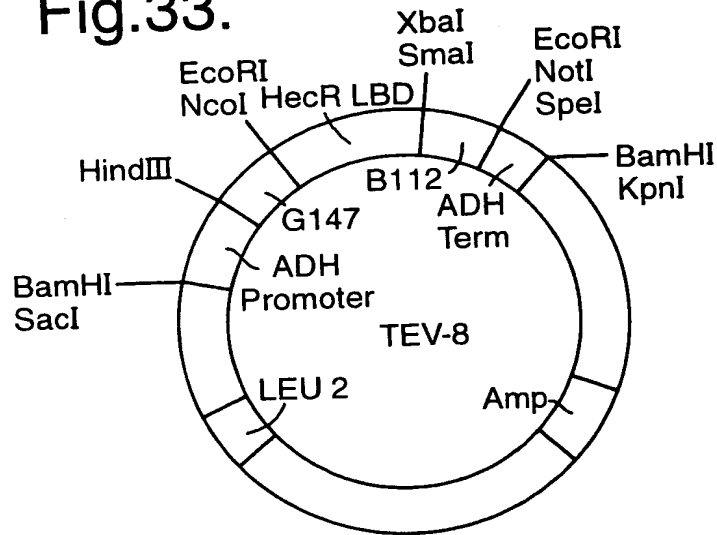


Fig.34.

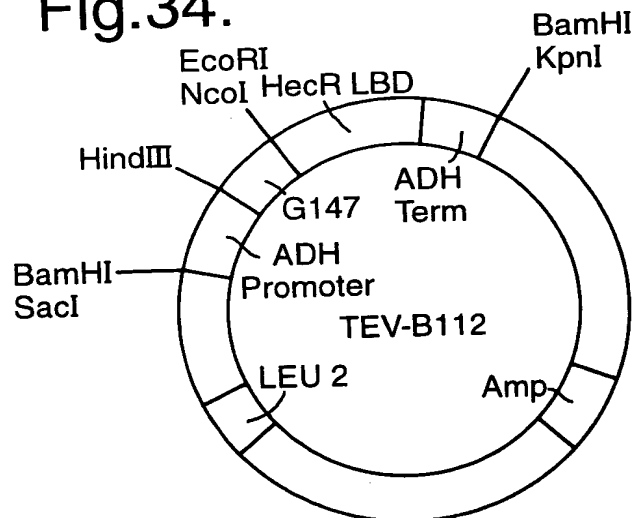


Fig.35.

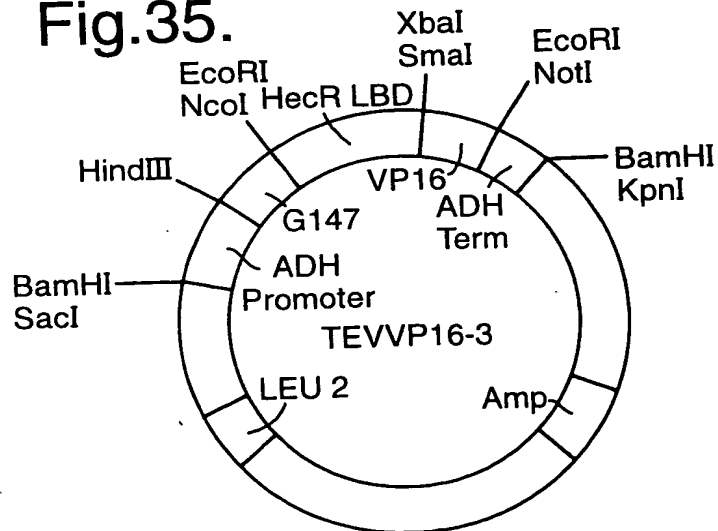


Fig.36.

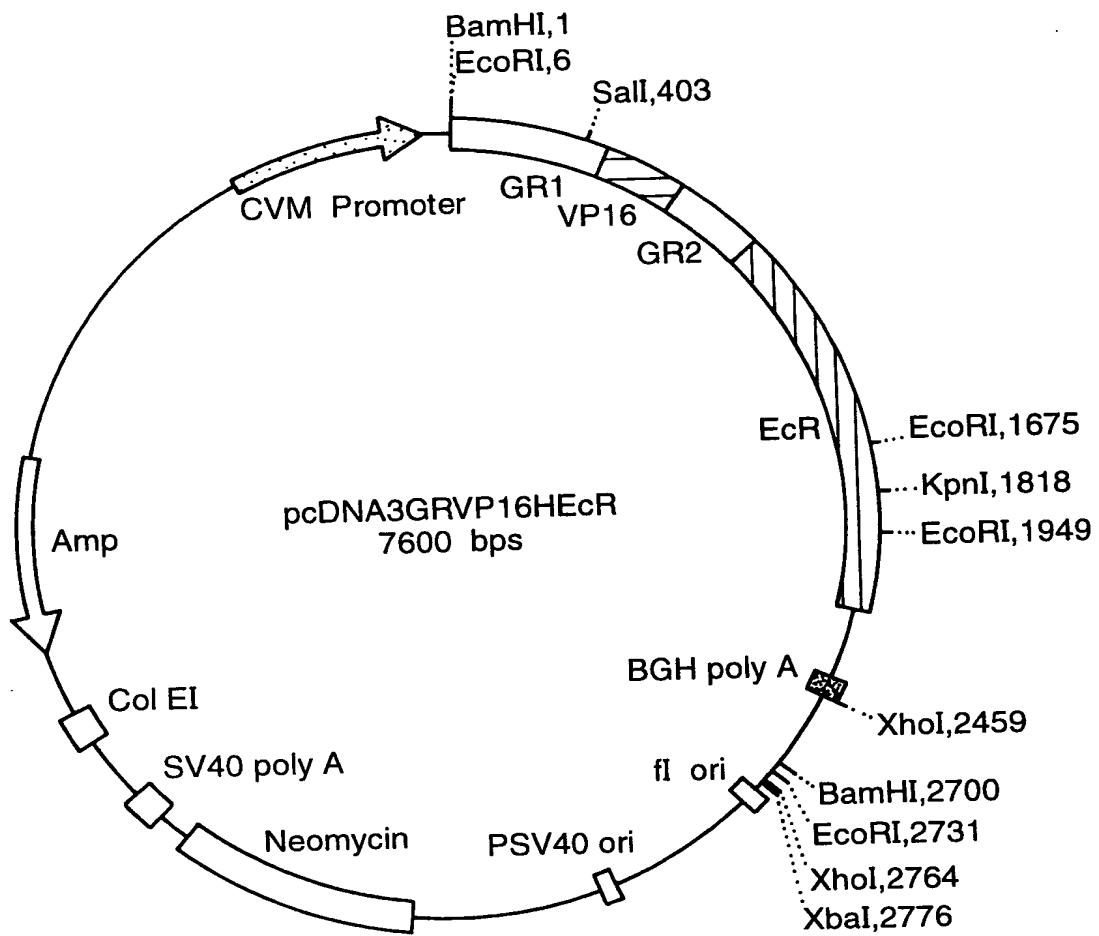


Fig.37.

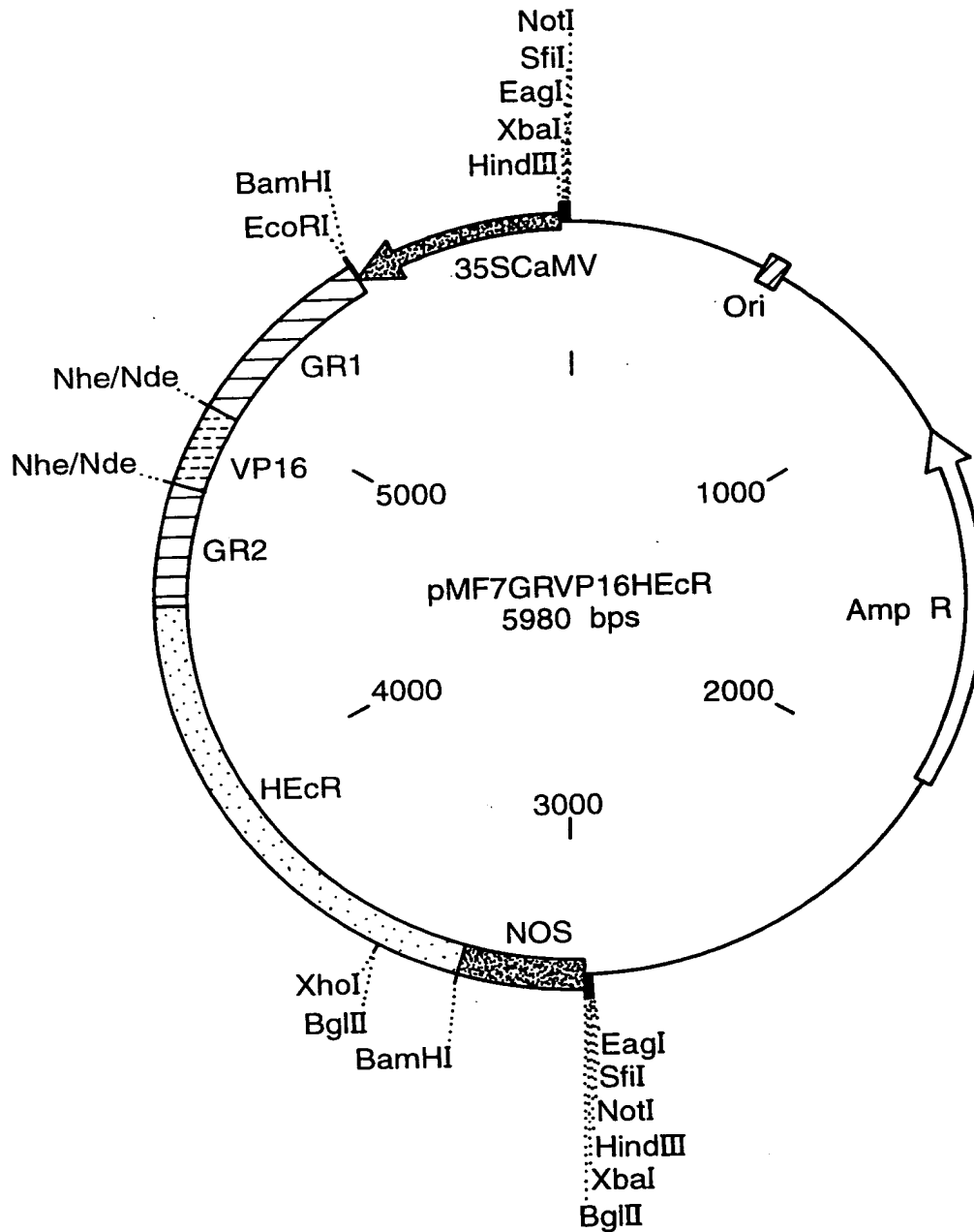
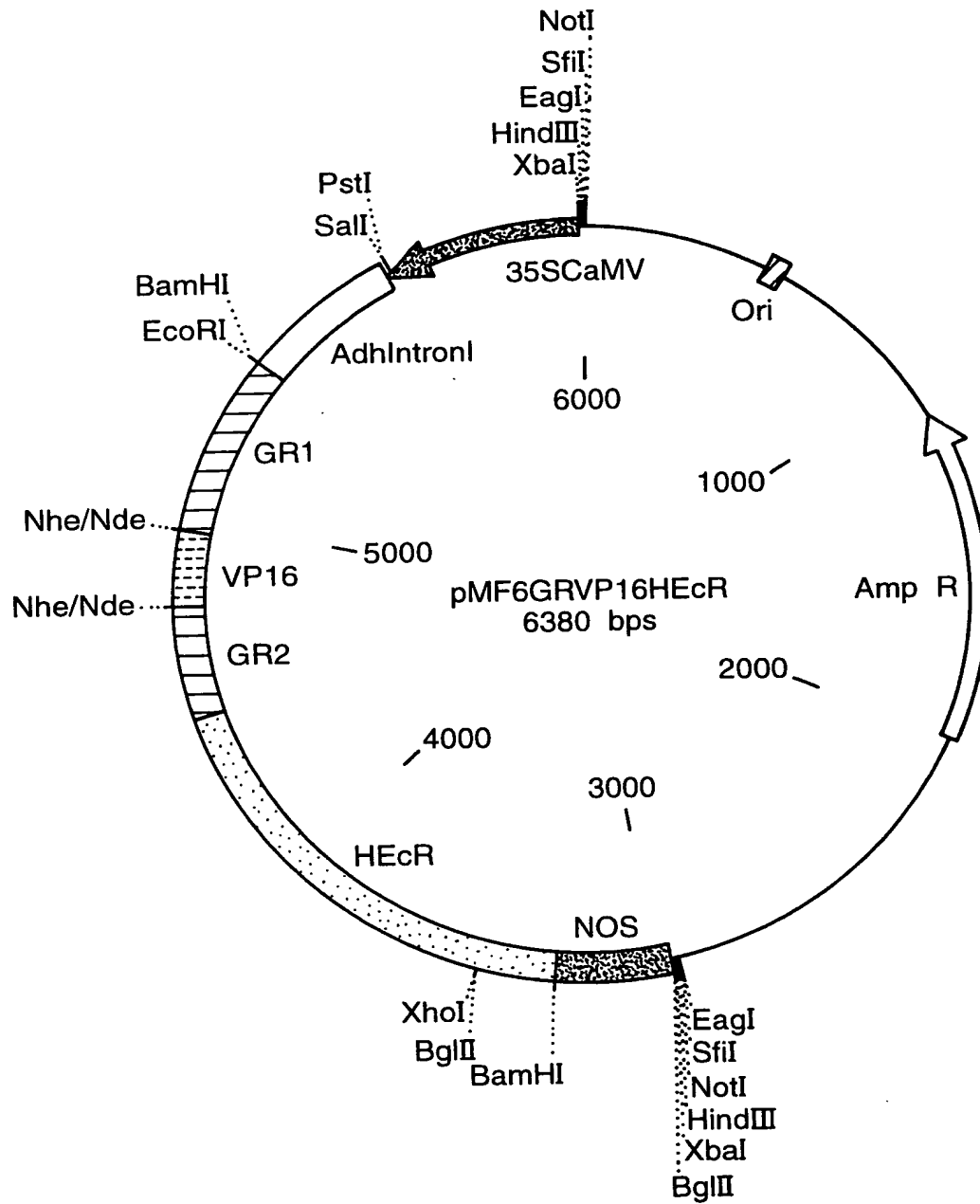
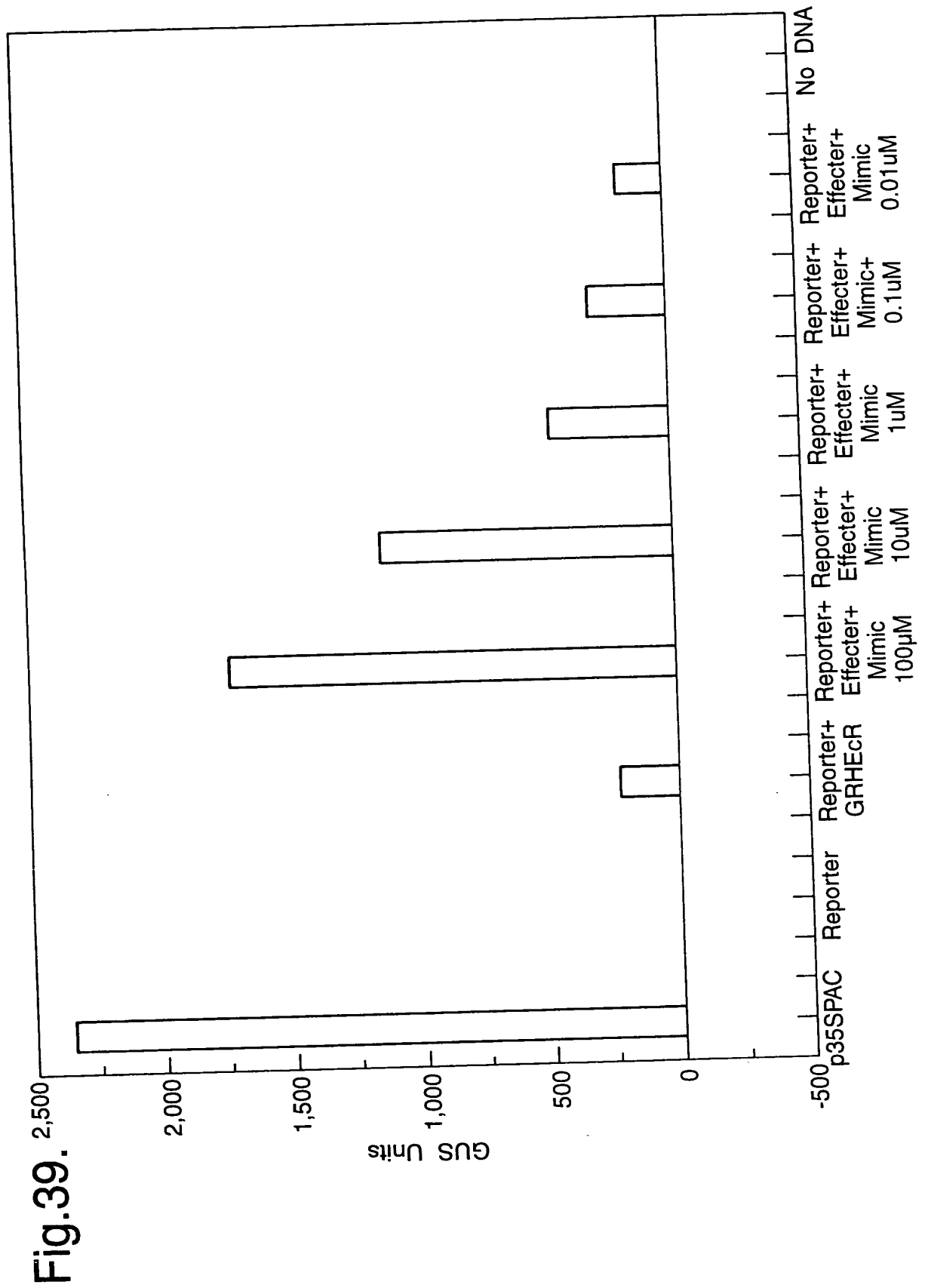


Fig.38.





Spodoptera exigua DNA sequence.

Fig.40.

Sequence ID 6

SPODOPTERA EXIGUA HINGE AND LIGAND BINDING DOMAINS

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 3 | 9 | 15 | 21 | 27 | 33 | 39 | 45 | | | | | | | | |
| | | | | | | | | | | | | | | | |
| 1 | AGG | CCG | GAG | TGC | GTG | CCA | GAA | AAC | CAG | TGT | GCA | ATG | AAA | AGG | |
| | TCC | GGC | CTC | ACG | CAC | CAC | GGT | CTT | TTG | GTC | ACA | CGT | TAC | TTT | TCC |
| 46 | AAA | GAG | AAA | AAG | GCA | CAA | AGG | GAA | AAA | GAC | AAG | TTG | CCA | GTC | AGT |
| | TTT | CTC | TTT | TTC | CGT | GTT | TCC | CTT | TTT | CTG | TTC | AAC | GGT | CAG | TCA |
| 91 | ACA | ACG | ACA | GTG | GAT | GAT | CAC | ATG | CCT | CCC | ATT | ATG | CAG | TGT | GAT |
| | TGT | TGC | TGT | CAC | CTA | CTA | GTG | TAC | GGA | GGG | TAA | TAC | GTC | ACA | CTA |
| 136 | CCA | CCG | CCT | CCA | GAG | GCC | GCA | AGA | ATT | CAC | GAG | GTG | GTG | CCA | CGA |
| | GGT | GGC | GGA | GGT | CTC | CGG | CGT | TCT | TAA | GTG | CTC | CAC | CAC | GGT | GCT |
| 181 | TTC | CTG | AAT | GAA | AAG | CTA | ATG | GAC | AGG | ACA | AGG | CTC | AAG | AAT | GTG |
| | AAG | GAC | TTA | CTT | TTC | GAT | TAC | CTG | TCC | TGT | TCC | GAG | TTC | TTA | CAC |
| 226 | CCC | CCT | CAC | TGC | CAA | CCA | GAA | GTC | CTT | AAT | AGC | GAG | GCT | GGT | CTG |
| | GGG | GGA | GTG | ACG | GTT | GGT | GGT | CAG | GAA | TTA | TCG | CTC | CGA | CCA | GAC |
| 271 | GTA | CCA | AGA | AGG | CTA | TGA | ACA | GCC | ATC | AGA | AGA | GGA | TCT | AAA | AAG |
| | CAT | GGT | TCT | TCC | GAT | ACT | TGT | CGG | TAG | TCT | TCT | CCT | AGA | TTT | TTC |

Fig.40 i.

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316 AGT CAC ACA GTC GGA TGA AGA CGA AGA AGA GTC GGA CAT GCC GTT
    TCA GTG TGT CAG CCT ACT TCT GCT TCT TCT CAG CCT GTA CGG CAA

361 CCG TCA GAT CAC CGA GAT GAC GAT CCT CAC AGT GCA GCT CAT TGT
    GGC AGT CTA GTG GCT CTA CTG CTA GGA GTG TCA CGT CGA GTA ACA

406 TGA ATT CGC TAA GGG CCT ACC AGC GTT CGC AAA GAT CTC ACA GTC
    ACT TAA GCG ATT CCC GGA TGG TCG CAA GCG TTT CTA GAG TGT CAG

451 GGA TCA GAT CAC ATT ATT AAA GGC CTG TTC GAG TGA GGT GAT GAT
    CCT AGT CTA GTG TAA TAA TTT CCG GAC AAG CTC ACT CCA CTA CTA

496 GTT GCG AGT AGC TCG GCG GTA CGA CGC GGC GAC AGA CAG CGT GTT
    CAA CGC TCA TCG AGC CGC CAT GCT GCG CCG CTG TCT GTC GCA CAA

541 GTT CGC CAA CAA CCA GGC GTA CAC CCG CGA CAA CTA CCG CAA GGC
    CAA GCG GTT GTT GGT CCG CAT GTG GGC GCT GAT GAT GGC GTT CCG

586 AGG CAT GGC CTA CGT CAT CGA GGA CCT GCT GCA CTT CTG CCG GTG
    TCC GTA CCG GAT GCA GTA GCT CCT GGA CGA CGT GAA GAC GGC CAC

631 CAT GTA CTC CAT GAT GAT GGA TAA CGT CCA CTA TGC ACT GCT CAC
    GTA CAT GAG GTA CTA CTA CCT ATT GCA GGT GAT ACG TGA CGA GTG

676 TGC CAT CGT CAT TTT CTC AGA CCG ACC CGG GCT TGA GCT AAC CCT
    ACG GTA GCA GTA AAA GAG TCT GGC TGG GCC CGA ACT CGA TTG GGA

721 GTT GGT GGA GGA GAT CCA GAG ATA TTA CCT GAA CAC GCT GCG GGT
    CAA CCA CCT CCT CTA GGT CTC TAT AAT GGA CTT GTG CGA CGC CCA

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Fig.40 ii. 766 GTA CAT CCT GAA CCA GAA CAG TCG GTC GCC GTG CTG CCC TGT CAT
CAT GTA GGA CTT GGT GGT CTT GTC AGC CAG CGG CAC GAC GAG GGG ACA GTA

811 CTA CGC TAA GAT CCT CGG CAT CCT GAC GGA GCT GCG GAC CCT GGG
GAT GCG ATT CTA GGA GCC GTA GGA CTG CCT CGA CGC CTG GGA CCC

856 CAT GCA GAA CTC CAA CAT GTG CAT CTC ACT CAA GCT GAA GAA CAG
GTA CGT CTT GAG GTT GTA CAC GTA GAG TGA GTT CGA CTT CTT GTC

901 GAA CGT GCC GCC GTT CTT CGA GGA TAT CTG GGA CGT CCT CGA GTA
CTT GCA CGG CGG CAA GAA GCT CCT ATA GAC CCT GCA GGA GCT CAT

946 AAA
TTT

Total number of bases is: 948.

Fig.41.

Sequence I.D. 7

sequence comparison between Heliothis 19R clone and SecR Taq clone

| | | |
|------|--|-------------------------------------|
| HECR | RPECVVPENQCAMKRKEKKAQREKDKLPVSTTTVDHMPPI | MCDDPPPEAARILECVQ |
| SECR | RPECVVPENQCAMKRKEKKAQREKDKLPVSTTTVDHMPPI | MCDDPPPPPEAARI |
| HECR | HEVVPFRFLNEKLMEQNRLKNVPPLTANQKSLIARLVWYQEGYE | QPSSEDLKRV |
| SECR | HEVVPFRFLNEKLMEQRLNRNVPPLTANQKSLIARLVWYQEGYE | QPSSEDLKRV |
| HECR | EDDESDMPFRQIT | EMTILTVQLIVEFAKGLPGFAKISQSDQITLLKAC |
| SECR | EDEESDMPFRQIT | EMTILTVQLIVEFAKGLPAFAKISQSDQITLLKAC |
| HECR | VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRC | MYSMMDNVHYALL |
| SECR | VARRYDAATDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRC | MYSMMDNVHYALL |
| HECR | TAIVIFSDRPGLEQLLVEEIQRYLNTLRVYILNQNSASPRGAVI | FGIILGILTEI |
| SECR | TAIVIFSDRPGLEQLLVEEIQRYLNTLRVYILNQNSRSPCCPVI | YAKILGILTEL |
| HECR | RTLGMQNSNMCISLKLKKRKLPPFLEEIDWDV | |
| SECR | RTLGMQNSNMCISLKLKNRNVPPFFEDIDWDV | |

Fig.42.

